



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 108672

TO: Manjunath N Rao
Location: CM1/10D01/10A11
Art Unit: 1652
Tuesday, November 25, 2003
Case Serial Number: 10/005306

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954



STIC-Biotech/ChemLib

108672

From: Chan, Christina
Sent: Wednesday, November 19, 2003 3:32 PM
To: Rao, Manjunath N.; STIC-Biotech/ChemLib
Subject: RE: RUSH sequence search request for 10/005,306

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Rao, Manjunath N.
Sent: Wednesday, November 19, 2003 2:48 PM
To: Chan, Christina
Subject: RUSH sequence search request for 10/005,306

Hello Christina,

Please authorize the request below as RUSH. The reason being this is an IFW due this bi-week.

From: Manjunath N. Rao
Art Unit 1652, Room 10A11
Mail Box in Room 10D 01
Phone: 306-5681

Date: 11-19-03

Please search the following as soon as possible for application with serial number

10/005306

1. SEQ ID NO: 9 against all commercial amino acid databases, issued patents/published applications database and pending application database. Please provide a print of all results.

If you have any questions please call me at the above phone number.

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 11/21
Date Completed: 11/25
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

Thanks

Manjunath N. Rao, Ph.D.
Biotechnology Patent Examiner
Art Unit 1652, Room 10A11
Mail Box in 10D01
Crystal Mall 1, USPTO.

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: November 21, 2003, 13:44:10 ; Search time 41 Seconds

(without alignments)

1006.559 Million cell updates/sec

Title: US-10-005-306-9

Perfect score: 1367

Sequence: 1 LKIAAFNIQTGETKMSNAT.....LSDLAQAIASHDFVPEVWLK 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_13Jun03.*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1367	100.0	260	19	AAW49937 Human mature DNase
2	1364	99.8	260	19	AAW49938 Human mature DNase
3	1362	99.6	260	17	AAW03666 Wild type human DN
4	1362	99.6	260	19	AAW49942 Human mature DNase
5	1362	99.6	260	19	AAW49929 Human mature DNase
6	1362	99.6	260	23	AAW51552 Human DNase I. Ho
7	1362	99.6	282	15	AAW45156 Human DNase I. Ho
8	1362	99.6	282	22	AAW52142 Human DNase I. enco
9	1362	99.6	282	24	ABP96647 Deoxyribonuclease

10	1362	99.6	515	22	AAW52162 Humanised HMFG-1 F
11	1362	99.6	517	22	AAW52154 Humanised HMFG-1 F
12	1362	99.6	519	22	AAW52164 Humanised HMFG-1 F
13	1362	99.6	521	22	AAW52163 Humanised HMFG-1 F
14	1362	99.6	525	22	AAW52166 Humanised HMFG-1 F
15	1362	99.6	527	22	AAW52155 Humanised HMFG-1 F
16	1362	99.6	529	22	AAW52168 Humanised HMFG-1 F
17	1362	99.6	531	22	AAW52167 Humanised HMFG-1 F
18	1362	99.6	729	22	AAW52158 Humanised HMFG-1 h
19	1362	99.6	730	22	AAW52157 Humanised HMFG-1 h
20	1362	99.6	731	22	AAW52156 Humanised HMFG-1 h
21	1362	99.6	739	22	AAW52161 Humanised HMFG-1 h
22	1362	99.6	740	22	AAW52160 Humanised HMFG-1 h
23	1362	99.6	741	22	AAW52159 Humanised HMFG-1 h
24	1360	99.5	260	17	AAW14386 Human DNase I vari
25	1360	99.5	260	22	AAW52143 Human DNase I enco
26	1359	99.4	260	17	AAW14398 Human DNase I vari
27	1359	99.4	260	17	AAW00692 Human DNase I vari
28	1358	99.3	260	17	AAW14408 Human DNase I vari
29	1358	99.3	260	17	AAW14374 Human DNase I vari
30	1358	99.3	260	17	AAW14375 Human DNase I vari
31	1358	99.3	260	17	AAW14402 Human DNase I vari
32	1358	99.3	260	17	AAW14363 Human DNase I vari
33	1358	99.3	260	19	AAW49939 Human mature DNase
34	1358	99.3	260	19	AAW49943 Human mature DNase
35	1358	99.3	260	19	AAW49930 Human mature DNase
36	1358	99.3	260	19	AAW49931 Human mature DNase
37	1358	99.3	282	15	AAW52662 Human DNase. Homo
38	1357	99.3	260	17	AAW14410 Human DNase I vari
39	1357	99.3	260	17	AAW14411 Human DNase I vari
40	1357	99.3	260	17	AAW14412 Human DNase I vari
41	1357	99.3	260	17	AAW14413 Human DNase I vari
42	1357	99.3	260	17	AAW14414 Human DNase I vari
43	1357	99.3	260	17	AAW14373 Human DNase I vari
44	1357	99.3	260	17	AAW14403 Human DNase I vari
45	1357	99.3	260	17	AAW14404 Human DNase I vari

ALIGNMENTS

RESULT 1

AAW49937
ID AAW49937 standard; protein; 260 AA.

XX AC AAW49937;

XX DT 05-JUN-1998 (first entry)

XX DE Human mature DNase I variant N74K.

XX XX Mature DNase I; variant; hyperactive; pulmonary disease; pneumonia;

XX KM systemic lupus erythematosus; cystic fibrosis; bronchitis; emphysema;

XX KW asthma; tuberculosis.

XX OS Homo sapiens.

XX OS Synthetic.

XX XX Key Location/Qualifiers

XX FT Misc-difference 74 /label= N74K

XX FT /note= "wild-type Asn is replaced by Lys"

XX XX KW09747751-A1.

XX XX 18-DEC-1997.

XX PD 09-JUN-1997; 97WO-US08517.

XX XX 14-JUN-1996; 96US-0663831.

XX PA (GETH) GENENTECH INC.

XX XX

PI Lazarus RA, Pan C;
XX WPI; 1998-052315/05.
XX Hyperactive variant of human DNaseI - useful to treat pulmonary
PT disease, e.g. cystic fibrosis and systemic lupus erythematosus
XX
XX Disclosure; Pages 25-26; 46pp; English.
XX
XX This is an hyperactive variant of the human mature DNase I. The wild-type
CC amino acid Asn at position 74 was substituted by Lys to create this
CC variant. The DNase I hyperactive variants differ from the wild-type
CC sequence by a single amino acid substitution and optionally one other
CC substitution. The hyperactive variant can be used to treat pulmonary
CC diseases, e.g. cystic fibrosis, systemic lupus erythematosus, bronchitis,
CC pneumonia, emphysema, asthma and tuberculosis, where it reduces the
CC viscoelasticity of pulmonary secretions. It can also be used as an
CC adjunct in the treatment of abscesses and many severe closed-space
CC infections, or in topical treatment of infectious lesions of the skin and
CC mucosa and burns, where it may improve the activity of antibiotics. The
CC variant can also be used to reduce and prevent the formation of DNA
CC containing immune complexes in a patient. Antibodies specific for the
CC variant can be used to detect/measure the variant in clinical samples,
CC and, when immobilised, to purify it from recombinant cell cultures.
CC Compared with wild type enzyme, the hyperactive variant has a greater
CC mucolytic activity and is more effective in degrading DNA generally. It
CC is less sensitive to inhibition by NaCl, so is more active under
CC physiological conditions.
XX
XX Sequence 260 AA;

Query Match 100.0%; Score 1367; DB 19; Length 260;
Best Local Similarity 100.0%; Pred. No. 3.1e-147;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGCTKSNATLVSYIVQILSRDYIALVQVDRSHLTAVGKLLDNLNQDAP 60
DB 1 LKIAAFNIQTGCTKSNATLVSYIVQILSRDYIALVQVDRSHLTAVGKLLDNLNQDAP 60
QY 61 DTHYVWSEPLGRSKYKERYLFVYRPQVSAVDVYVDDGCEPCGNDTFNREPAIVRFS 120
DB 61 DTHYVWSEPLGRSKYKERYLFVYRPQVSAVDVYVDDGCEPCGNDTFNREPAIVRFS 120
QY 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
DB 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVDPDSALPFFQAYG 240
DB 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVDPDSALPFFQAYG 240
QY 241 LSDQLAQAISSDHYFVEVWMLK 260
DB 241 LSDQLAQAISSDHYFVEVWMLK 260

RESULT 2
AAW49938
ID AAW49938 standard; protein; 260 AA.
XX
XX AAW49938;
XX
XX 05-JUN-1998 (first entry)
DE Human mature DNase I variant N74R.
XX
XX Mature DNase I; variant; hyperactive; pulmonary disease; pneumonia;
KW systemic lupus erythematosus; cystic fibrosis; bronchitis; emphysema;
KW asthma; tuberculosis.
XX
XX Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
Misc-difference 74 /label= N74R
/note= "wild-type Asn is replaced by Arg"
XX W09747751-A1.
XX 18-DEC-1997.
XX
XX 09-JUN-1997; 97WO-0508517.
XX
XX 14-JUN-1996; 96US-0663831.
XX (GETH) GENENTECH INC.
XX
XX Lazarus RA, Pan C;
XX WPI; 1998-052315/05.
XX
XX Hyperactive variant of human DNaseI - useful to treat pulmonary
PT disease, e.g. cystic fibrosis and systemic lupus erythematosus
XX
XX Disclosure; Pages 26-27; 46pp; English.

This is an hyperactive variant of the human mature DNase I. The wild-type
CC amino acid Asn at position 74 was substituted by Arg to create this
CC variant. The DNase I hyperactive variants differ from the wild-type
CC sequence by a single amino acid substitution and optionally one other
CC substitution. The hyperactive variant can be used to treat pulmonary
CC diseases, e.g. cystic fibrosis, systemic lupus erythematosus, bronchitis,
CC pneumonia, emphysema, asthma and tuberculosis, where it reduces the
CC viscoelasticity of pulmonary secretions. It can also be used as an
CC adjunct in the treatment of abscesses and many severe closed-space
CC infections, or in topical treatment of infectious lesions of the skin and
CC mucosa and burns, where it may improve the activity of antibiotics. The
CC variant can also be used to reduce and prevent the formation of DNA
CC containing immune complexes in a patient. Antibodies specific for the
CC variant can be used to detect/measure the variant in clinical samples,
CC and, when immobilised, to purify it from recombinant cell cultures.
CC Compared with wild type enzyme, the hyperactive variant has a greater
CC mucolytic activity and is more effective in degrading DNA generally. It
CC is less sensitive to inhibition by NaCl, so is more active under
CC physiological conditions.

Query Match 99.8%; Score 1364; DB 19; Length 260;
Best Local Similarity 99.6%; Pred. No. 6.9e-147;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGCTKSNATLVSYIVQILSRDYIALVQVDRSHLTAVGKLLDNLNQDAP 60
DB 1 LKIAAFNIQTGCTKSNATLVSYIVQILSRDYIALVQVDRSHLTAVGKLLDNLNQDAP 60
QY 61 DTHYVWSEPLGRSKYKERYLFVYRPQVSAVDVYVDDGCEPCGNDTFNREPAIVRFS 120
DB 61 DTHYVWSEPLGRSKYKERYLFVYRPQVSAVDVYVDDGCEPCGNDTFNREPAIVRFS 120
QY 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
DB 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVDPDSALPFFQAYG 240
DB 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVDPDSALPFFQAYG 240
QY 241 LSDQLAQAISSDHYFVEVWMLK 260
DB 241 LSDQLAQAISSDHYFVEVWMLK 260

RESULT 3
AAW03666

ID AAW03666 standard; protein; 260 AA.
 XX AAW03666;
 AC
 XX
 DT 02-MAY-1997 (first entry)
 XX
 DE Wild type human DNase I.
 XX
 XX human mature DNase I; actin-resistant variant; treat; pulmonary disease;
 KW disorder; cystic fibrosis; chronic bronchitis; viscoelasticity; viscous;
 KW consistency; asthma; systemic lupus erythematosus; in vitro; assay.
 XX
 XX Homo sapiens.
 OS
 XX W09626279-A1.
 XX
 XX 29-AUG-1996.
 XX
 XX 21-FEB-1996; 96WO-US02421.
 XX
 XX 10-OCT-1995; 95US-0540527.
 PR 24-FEB-1995; 95WO-US02366.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Lazarus RA, Shak S, Ulmer JS;
 PT WPI; 1996-402370/40.
 DR
 XX New actin-resistant human DNaseI variants - used for reducing the
 PT viscous consistency of DNA-contg. material, e.g. for treating
 PT chronic bronchitis or cystic fibrosis
 PS
 XX Claim 4; Fig 1; 149pp; English.
 XX
 CC The present sequence is that of human mature DNase I. Actin-resistant
 CC variants of human DNase I (see AAW14323-421) are used to treat pulmonary
 CC diseases or disorders esp. cystic fibrosis or chronic bronchitis. They
 CC can be used for reducing the viscoelasticity or viscous consistency of
 CC DNA-contg. material in a patient. They can be used for treating e.g.
 CC acute or chronic bronchial pulmonary disease, asthma, systemic lupus
 CC erythematosus. They can also be used in in vitro diagnostic assays of a
 CC viscous material from a patient to measure the amt. of actin present and
 CC determine whether the patient is an appropriate candidate for treatment
 CC with an actin-resistant DNase I variant. Because the variants have
 CC reduced affinity for actin, their DNA hydrolytic activity is less
 CC inhibited in the presence of actin and so these variants have greater
 CC mucolytic activity in the presence of actin as compared to native human
 CC DNase I.
 XX
 XX Sequence 260 AA;
 SQ
 Query Match 99.6%; Score 1362; DB 17; Length 260;
 Best Local Similarity 99.6%; Pred. No. 1.2e-146;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKIAAFNIQTGFTGMSNATLVSVYQILSRDIALVQVVRDLSHLTAVGKLLDNLDQAP 60
 DB 1 LKIAAFNIQTGFTGMSNATLVSVYQILSRDIALVQVVRDLSHLTAVGKLLDNLDQAP 60
 QY 61 DTYHVYVSEPLGRSKYKERYLFVYRPPQVSAVDVSYDDGCEPCGNDTFNREPAIVRFFS 120
 DB 61 DTYHVYVSEPLGRSKYKERYLFVYRPPQVSAVDVSYDDGCEPCGNDTFNREPAIVRFFS 120
 QY 121 RFTVEVREPAIVPLHAAPGDAVAEIDALYDVYLDVQVKEWGLDVMGMDFNAGCSYVRPSQ 180
 DB 121 RFTVEVREPAIVPLHAAPGDAVAEIDALYDVYLDVQVKEWGLDVMGMDFNAGCSYVRPSQ 180
 QY 181 WSSIRLWTSPTFQMLIPDSATTTPTHTCAVDRTVAVAGMLRGAVVDPDSALPENFQAAYG 240
 DB 181 WSSIRLWTSPTFQMLIPDSATTTPTHTCAVDRTVAVAGMLRGAVVDPDSALPENFQAAYG 240
 QY 241 LSDQLAQAI SDHYPEVMK 260

DB 241 LSDQLAQAI SDHYPEVMK 260
 RESULT 4
 AAW49942
 ID AAW49942 standard; protein; 260 AA.
 XX
 AC AAW49942;
 XX
 DT 05-JUN-1998 (first entry)
 XX
 XX Human mature DNase I variant E13R:N74K.
 DE
 XX Mature DNase I; variant; hyperactive; pulmonary disease; pneumonia;
 KW systemic lupus erythematosus; cystic fibrosis; bronchitis; emphysema;
 KW asthma; tuberculosis.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 13 /label= E13R
 FT /note= "wild-type Glu is replaced by Arg"
 FT Misc-difference 74 /label= N74K
 FT /note= "wild-type Asn is replaced by Lys"
 FT
 XX W09747751-A1.
 PN
 XX 18-DEC-1997.
 PD
 XX 09-JUN-1997; 97WO-US08517.
 PF
 XX 14-JUN-1996; 96US-0663831.
 PR (GETH) GENENTECH INC.
 XX
 XX Lazarus RA, Pan C;
 PI WPI; 1998-052315/05.
 DR
 XX Hyperactive variant of human DNaseI - useful to treat pulmonary
 PT disease, e.g. cystic fibrosis and systemic lupus erythematosus
 PT
 XX Disclosure; Pages 30-31; 46pp; English.
 PS
 XX This is an hyperactive variant of the human mature DNase I. This double
 CC mutant is created by substitutions of wild-type amino acids Glu and Asn
 CC at positions 13 and 74 by Arg and Lys respectively. The hyperactive
 CC variant can be used to treat pulmonary diseases, e.g. cystic fibrosis,
 CC systemic lupus erythematosus, bronchitis, pneumonia, emphysema, asthma
 CC and tuberculosis, where it reduces the viscoelasticity of pulmonary
 CC secretions. It can also be used as an adjunct in the treatment of
 CC abscesses and many severe closed-space infections, or in topical
 CC treatment of infectious lesions of the skin and mucosa and burns, where
 CC it may improve the activity of antibiotics. The variant can also be used
 CC to reduce and prevent the formation of DNA containing immune complexes in
 CC a patient. Antibodies specific for the variant can be used to detect/
 CC measure the variant in clinical samples, and, when immobilised, to purify
 CC it from recombinant cell cultures. Compared with wild type enzyme, the
 CC hyperactive variant has a greater mucolytic activity and is more
 CC effective in degrading DNA generally. It is less sensitive to inhibition
 CC by NaCl, so is more active under physiological conditions.
 XX
 XX Sequence 260 AA;
 SQ
 Query Match 99.6%; Score 1362; DB 19; Length 260;
 Best Local Similarity 99.6%; Pred. No. 1.2e-146;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKIAAFNIQTGFTGMSNATLVSVYQILSRDIALVQVVRDLSHLTAVGKLLDNLDQAP 60

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Db 1 LKIAAFNIQTGRTKSNATLVSYIVQILSRDYIALVQEVDRSHLTAVGKLLDNLNQDAP 60
QY 61 DTYHYVVSEPLGRKSKYERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNRBPALVRFPS 120
Db 61 DTYHYVVSEPLGRKSKYERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNRBPALVRFPS 120
QY 121 RFTVEVREFAIPLHAAFGDAVAEIDALYDVLDVQEKWGLDVMKGFNAGCSYVRPSQ 180
Db 121 RFTVEVREFAIPLHAAFGDAVAEIDALYDVLDVQEKWGLDVMKGFNAGCSYVRPSQ 180
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVDPDSALPFFNQAAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVDPDSALPFFNQAAYG 240
QY 241 LSDQLAQAIISDHPYVEVMLK 260
Db 241 LSDQLAQAIISDHPYVEVMLK 260

RESULT 5
AAW49929
ID AAW49929 standard; protein; 260 AA.
AC AAW49929;
XX
DT 05-JUN-1998 (first entry)
XX
DE Human mature DNase I.
XX
KW Mature DNase I; variant; hyperactive; pulmonary disease; pneumonia;
KW systemic lupus erythematosus; cystic fibrosis; bronchitis; emphysema;
KW asthma; tuberculosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 9
FT /note= "Gln at this position can be substituted
FT to create a variant"
FT Misc-difference 13
FT /note= "Glu at this position can be substituted
FT to create a variant"
FT Misc-difference 14
FT /note= "Thr at this position can be substituted
FT to create a variant"
FT Misc-difference 44
FT /note= "His at this position can be substituted
FT to create a variant"
FT Misc-difference 74
FT /note= "Asn at this position can be substituted
FT to create a variant"
FT Misc-difference 75
FT /note= "Ser at this position can be substituted
FT to create a variant"
FT Misc-difference 205
FT /note= "Thr at this position can be substituted
FT to create a variant"
XX
PN WO9747751-A1.
XX
PD 18-DEC-1997.
XX
PF 09-JUN-1997; 97WO-US08517.
XX
PR 14-JUN-1996; 96US-0663831.
XX
PA (GETH ) GENENTECH INC.
XX
PI Lazarus RA, Pan C;
XX
DR WPI; 1998-052315/05.
XX
PD 15-NOV-2001.

Hyperactive variant of human DNaseI - useful to treat pulmonary
disease, e.g. cystic fibrosis and systemic lupus erythematosus
Disclosure; Fig 1; 46pp; English.
This sequence represents the human mature DNase I. This sequence can be
substituted at amino acid positions Gln9, Glu13, Thr14, His44, Asn74,
Ser75 or Thr205 (residues involved in DNA binding) to create hyperactive
variants of DNase I. The variants differ from the wild-type DNase I
sequence by a single amino acid substitution and optionally one other
substitution. The hyperactive variant can be used to treat pulmonary
diseases, e.g. cystic fibrosis, systemic lupus erythematosus, bronchitis,
pneumonia, emphysema, asthma and tuberculosis, where it reduces the
viscoelasticity of pulmonary secretions. It can also be used as an
adjuvant in the treatment of abscesses and many severe closed-space
infections, or in topical treatment of infectious lesions of the skin and
mucosa and burns, where it may improve the activity of antibiotics. The
variant can also be used to reduce and prevent the formation of DNA
containing immune complexes in a patient. Antibodies specific for the
variant can be used to detect/measure the variant in clinical samples,
and, when immobilised, to purify it from recombinant cell cultures.
Compared with wild type enzyme, the hyperactive variant has a greater
mucolytic activity and is more effective in degrading DNA generally. It
is less sensitive to inhibition by NaCl, so is more active under
physiological conditions.
Query Match 99.6%; Score 1362; DB 19; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.2e-146;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGRTKSNATLVSYIVQILSRDYIALVQEVDRSHLTAVGKLLDNLNQDAP 60
Db 1 LKIAAFNIQTGRTKSNATLVSYIVQILSRDYIALVQEVDRSHLTAVGKLLDNLNQDAP 60
QY 61 DTYHYVVSEPLGRKSKYERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNRBPALVRFPS 120
Db 61 DTYHYVVSEPLGRKSKYERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNRBPALVRFPS 120
QY 121 RFTVEVREFAIPLHAAFGDAVAEIDALYDVLDVQEKWGLDVMKGFNAGCSYVRPSQ 180
Db 121 RFTVEVREFAIPLHAAFGDAVAEIDALYDVLDVQEKWGLDVMKGFNAGCSYVRPSQ 180
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVDPDSALPFFNQAAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVDPDSALPFFNQAAYG 240
QY 241 LSDQLAQAIISDHPYVEVMLK 260
Db 241 LSDQLAQAIISDHPYVEVMLK 260

RESULT 6
AAW51552
ID AAW51552 standard; protein; 260 AA.
XX
AC AAW51552;
XX
DT 14-JAN-2002 (first entry)
XX
DE Human DNase I.
XX
KW Human; DNase I; respiratory; mucolytic; antiasthmatic; dermatological;
KW immunosuppressant; antiinflammatory; actin-resistant; variant;
KW cystic fibrosis; chronic bronchitis; pneumonia; bronchiectasis;
KW emphysema; asthma; systemic lupus erythematosus; DNA hydrolysis.
XX
OS Homo sapiens.
XX
PN US2001041360-A1.
XX
PD 15-NOV-2001.

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XX PF 28-FEB-2001; 2001US-0796774.
XX PR 10-OCT-1995; 95US-0540527.
XX PR 15-SEP-1997; 97US-0929995.
XX PR 24-FEB-1995; 95NO-US02366.
XX PR 24-MAR-1996; 96US-0403873.
XX PA (GETH ) GENENTECH INC.
XX PI Lazarus RA, Shak S, Ulmer JS;
XX PI WPI; 2002-017217/02.
XX DR
XX PF Actin-resistant variants of human DNase I and encoding nucleic acids,
XX PT useful for treating cystic fibrosis and chronic bronchitis -
XX XX
XX PS Claim 4; Fig 1; 25pp; English.
XX CC The invention relates to human DNase I actin-resistant variants and
XX CC the nucleic acids that encode them. The variants are used for the
XX CC treatment of cystic fibrosis and chronic bronchitis, pneumonia,
XX CC bronchiectasis, emphysema, asthma, and systemic lupus erythematosus.
XX CC DNase I reduces the viscoelasticity of pulmonary secretions (mucus) in
XX CC such diseases as pneumonia and cystic fibrosis, therefore aiding in the
XX CC clearing of respiratory airways. In the presence of actin, the
XX CC DNA-hydrolytic activity of DNase I is inhibited. Actin-resistant DNase I
XX CC variants have decreased ability to bind actin, but still have mucolytic
XX CC activity and in some cases have increased mucolytic activity as compared
XX CC to native human DNase I because their DNA-hydrolytic activity is
XX CC less inhibited. The present sequence is native human DNase I.
XX XX
XX SQ Sequence 260 AA;
XX
XX Query Match 99.6%; Score 1362; DB 23; Length 260;
XX Best Local Similarity 99.6%; Pred. No. 1.2e-146;
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 LKIAAFNIQTGCTKMSNATLSYIVQLSRDYDIALVOEVRDLSHTAVGKLLDNLNQDAP 60
Db 1 LKIAAFNIQTGCTKMSNATLSYIVQLSRDYDIALVOEVRDLSHTAVGKLLDNLNQDAP 60
QY 61 DTYHYVWSEPLGRKSYKERYLFVYRPDQVSAVDSVYDDGCEPCGNDTFNREPAIVRFFS 120
Db 61 DTYHYVWSEPLGRKSYKERYLFVYRPDQVSAVDSVYDDGCEPCGNDTFNREPAIVRFFS 120
QY 121 RFTVREFAIVPLHAAPGDVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
Db 121 RFTVREFAIVPLHAAPGDVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFNFQAAAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFNFQAAAYG 240
QY 241 LSDQLAQAI SDHYFVVEWMLK 260
Db 241 LSDQLAQAI SDHYFVVEWMLK 260

RESULT 7
AAR45356
ID AAR45356 standard; Protein; 282 AA.
XX AC AAR45356;
XX XX
XX DT 25-MAR-2003 (updated)
XX TT 22-JUN-1994 (first entry)
XX XX
XX DE Human DNase I.
XX KW DNase; non-deamidated; deamidated; pulmonary distress;
XX KW cystic fibrosis; chronic bronchitis; emphysema; pneumonia;
XX KW asthma; tuberculosis; fungal infection.

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XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT /label= sig_peptide
XX FT /label= mat_protein
XX FT 23..282
XX FT /label= mat_protein
XX PN W09325670-A1.
XX XX
XX PD 23-DEC-1993.
XX XX
XX PF 28-MAY-1993; 93WO-US05136.
XX PR 08-JUN-1992; 92US-0895300.
XX PA (GETH ) GENENTECH INC.
XX PI Frenz J, Shire SJ, Sliwkowski MB;
XX DR WPI; 1994-007528/01.
XX DR N-PSDB; AAQ54429.
XX PT Purified forms of non-deamidated and deamidated human DNase - for
XX PT treatment of pulmonary distress, cystic fibrosis, chronic
XX PT bronchitis, emphysema, pneumonia, asthma, tuberculosis and fungal
XX PT infections
XX PS Disclosure; Fig 1; 38pp; English.
XX CC Two components of a recombinant prepn. of DNase are identified and
XX CC characterised. A separation method and uses of these components
XX CC are given in the specification.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 282 AA;
XX
XX Query Match 99.6%; Score 1362; DB 15; Length 282;
XX Best Local Similarity 99.6%; Pred. No. 1.3e-146;
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 LKIAAFNIQTGCTKMSNATLSYIVQLSRDYDIALVOEVRDLSHTAVGKLLDNLNQDAP 60
Db 23 LKIAAFNIQTGCTKMSNATLSYIVQLSRDYDIALVOEVRDLSHTAVGKLLDNLNQDAP 82
QY 61 DTYHYVWSEPLGRKSYKERYLFVYRPDQVSAVDSVYDDGCEPCGNDTFNREPAIVRFFS 120
Db 83 DTYHYVWSEPLGRKSYKERYLFVYRPDQVSAVDSVYDDGCEPCGNDTFNREPAIVRFFS 142
QY 121 RFTVREFAIVPLHAAPGDVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
Db 143 RFTVREFAIVPLHAAPGDVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 202
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFNFQAAAYG 240
Db 203 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFNFQAAAYG 262
QY 241 LSDQLAQAI SDHYFVVEWMLK 260
Db 263 LSDQLAQAI SDHYFVVEWMLK 282

RESULT 8
AAM52142
ID AAM52142 standard; Protein; 282 AA.
XX AC AAM52142;
XX XX
XX DT 05-FEB-2002 (first entry)
XX DE Human DNase I encoding polynucleotide 1.
XX XX

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KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
 XX Homo sapiens.
 XX WO200174905-A1.
 XX PD 11-OCT-2001.
 XX 26-MAR-2001; 2001WO-GB01324.
 XX 03-APR-2000; 2000GB-0008049.
 PR 02-OCT-2000; 2000US-237159P.
 XX (ANTI-) ANTISOMA RES LTD.
 XX Young RJ;
 PI WPI; 2001-662969/76.
 DR Novel compound used to treat cancer has target cell-specific portion
 PT comprising humanised monoclonal antibody having specificity for
 PT polymorphic epithelial mucin, and cytotoxic portion having
 PT endonucleolytic activity -
 XX Disclosure; Figure 1; 176pp; English.
 XX The invention relates to a compound which comprises a target
 CC cell-specific portion, comprising an humanised monoclonal antibody,
 CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis.
 XX Sequence 282 AA;
 SQ Query Match 99.6%; Score 1362; DB 22; Length 282;
 Best Local Similarity 99.6%; Pred. No. 1.3e-146;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKIAAFNIQTGETKMSNATLSYIVQILSRVDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
 Db 23 LKIAAFNIQTGETKMSNATLSYIVQILSRVDIALVQEVDRSHLTAVGKLLDNLNQDAP 82
 QY 61 DTYHYVVSPEPLGRKSYKERYLFVYRPDQVSADSVYDDGCEPCGNDTFNREPAIVRFFS 120
 Db 83 DTYHYVVSPEPLGRKSYKERYLFVYRPDQVSADSVYDDGCEPCGNDTFNREPAIVRFFS 142
 QY 121 RFTVEVREFAIPLHAAPGDAVAEIDALYDVLDVQEKWGLEVDVLMGDFNAGCSYVRPSQ 180
 Db 143 RFTVEVREFAIPLHAAPGDAVAEIDALYDVLDVQEKWGLEVDVLMGDFNAGCSYVRPSQ 202
 QY 181 WSSIRLWTSPTFQWMLIPDSADTTATPTHCAYDRIWVAGMLRGAVVPDSALPFFNFOAAAYG 240
 Db 203 WSSIRLWTSPTFQWMLIPDSADTTATPTHCAYDRIWVAGMLRGAVVPDSALPFFNFOAAAYG 262
 QY 241 LSDQLAQALSDHYPEVVMK 260
 Db 263 LSDQLAQALSDHYPEVVMK 282
 RESULT 9
 ABP96647
 ID ABP96647 standard; Protein; 282 AA.
 AC ABP96647;
 XX 30-MAY-2003 (first entry)
 DT Deoxyribonuclease I protein SEQ ID NO:3.
 DE Deoxyribonuclease I; DNase-I; deoxyribonuclease; enzyme;
 XX Deoxyribonuclease I; DNase-I; deoxyribonuclease; enzyme;
 KW

KW respiratory system disease.
 XX Unidentified.
 XX CN1366042-A.
 XX PD 28-AUG-2002.
 XX 19-JAN-2001; 2001CN-0101653.
 XX 19-JAN-2001; 2001CN-0101653.
 PA (HUAD-) HUADA GENE RES CENT BEIJING.
 XX Liu S, Feng X, Wang C;
 PI WPI; 2003-240395/24.
 DR N-PSDB; ACC44599.
 XX Process for preparing recombinant deoxyribonuclease I -
 PT Example 1; Page 18-19 (disclosure); 23pp; Chinese.
 XX The present invention describes a process for preparing recombinant
 CC deoxyribonuclease I (DNase-I) with biological activity. DNase-I can
 CC be used to treat diseases in the respiratory system. The present
 CC sequence represents a DNase-I which is given in the exemplification of
 CC the present invention.
 XX Sequence 282 AA;
 SQ Query Match 99.6%; Score 1362; DB 24; Length 282;
 Best Local Similarity 99.6%; Pred. No. 1.3e-146;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKIAAFNIQTGETKMSNATLSYIVQILSRVDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
 Db 23 LKIAAFNIQTGETKMSNATLSYIVQILSRVDIALVQEVDRSHLTAVGKLLDNLNQDAP 82
 QY 61 DTYHYVVSPEPLGRKSYKERYLFVYRPDQVSADSVYDDGCEPCGNDTFNREPAIVRFFS 120
 Db 83 DTYHYVVSPEPLGRKSYKERYLFVYRPDQVSADSVYDDGCEPCGNDTFNREPAIVRFFS 142
 QY 121 RFTVEVREFAIPLHAAPGDAVAEIDALYDVLDVQEKWGLEVDVLMGDFNAGCSYVRPSQ 180
 Db 143 RFTVEVREFAIPLHAAPGDAVAEIDALYDVLDVQEKWGLEVDVLMGDFNAGCSYVRPSQ 202
 QY 181 WSSIRLWTSPTFQWMLIPDSADTTATPTHCAYDRIWVAGMLRGAVVPDSALPFFNFOAAAYG 240
 Db 203 WSSIRLWTSPTFQWMLIPDSADTTATPTHCAYDRIWVAGMLRGAVVPDSALPFFNFOAAAYG 262
 QY 241 LSDQLAQALSDHYPEVVMK 260
 Db 263 LSDQLAQALSDHYPEVVMK 282
 RESULT 10
 AAM52162
 ID AAM52162 standard; Protein; 515 AA.
 XX AAM52162;
 AC AAM52162;
 XX 05-FEB-2002 (first entry)
 DT Humanised HMEG-1 Fd/DNase I fusion protein 2.
 XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200174905-A1.
 PN

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XX PD 11-OCT-2001.
XX PD 26-MAR-2001; 2001WO-GB01324.
XX PF 03-APR-2000; 2000GB-0008049.
XX PR 02-OCT-2000; 2000US-237159P.
XX PA (ANTI-) ANTISOMA RES LTD.
XX PI Young RJ;
XX PI WPI; 2001-662969/76.
XX DR Novel compound used to treat cancer has target cell-specific portion
XX PT comprising humanised monoclonal antibody having specificity for
XX PT polymorphic epithelial mucin, and cytotoxic portion having
XX PT endonucleolytic activity -
XX PS Claim 20; Figure 13; 176pp; English.
XX CC The invention relates to a compound which comprises a target
XX CC cell-specific portion, comprising an humanised monoclonal antibody,
XX CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX CC binding fragment and a cytotoxic portion having endonucleolytic activity,
XX CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
XX CC compound has cytostatic activity useful for treating cancer and acting as
XX CC a potential inducer of apoptosis.
XX SQ Sequence 515 AA;

Query Match 99.6%; Score 1362; DB 22; Length 515;
Best Local Similarity 99.6%; Pred. No. 3.2e-146;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 60
DB 256 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 315

QY 61 DTYHYVSEPLGRKSYKERYLFVYRPDOVSADVSYVDGCGPCGNDTFNREPAIVRFFS 120
DB 316 DTYHYVSEPLGRKSYKERYLFVYRPDOVSADVSYVDGCGPCGNDTFNREPAIVRFFS 375

QY 121 RFEVREPAIVPLHAAPGDVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
DB 376 RFEVREPAIVPLHAAPGDVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 435

QY 181 WSSIRLWTSPTFQWLIIPDSADTTATPTHCAYDRIVVAGMLLRGAVVDPDSALPFNFQAYG 240
DB 436 WSSIRLWTSPTFQWLIIPDSADTTATPTHCAYDRIVVAGMLLRGAVVDPDSALPFNFQAYG 495

QY 241 LSDQLAQAIISDHPYVEVWLK 260
DB 496 LSDQLAQAIISDHPYVEVWLK 515

RESULT 11
AAM52154
ID AAM52154 standard; Protein; 517 AA.
XX AC AAM52154;
XX AC AAM52154;
DT 05-FEB-2002 (first entry)
XX DE Humanised HMFG-1 Fd/DNase I fusion protein 1.
XX KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
XX KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200174905-A1.

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XX PD 11-OCT-2001.
XX PD 26-MAR-2001; 2001WO-GB01324.
XX PF 03-APR-2000; 2000GB-0008049.
XX PR 02-OCT-2000; 2000US-237159P.
XX PA (ANTI-) ANTISOMA RES LTD.
XX PI Young RJ;
XX PI WPI; 2001-662969/76.
XX DR Novel compound used to treat cancer has target cell-specific portion
XX PT comprising humanised monoclonal antibody having specificity for
XX PT polymorphic epithelial mucin, and cytotoxic portion having
XX PT endonucleolytic activity -
XX PS Claim 20; Figure 5; 176pp; English.
XX CC The invention relates to a compound which comprises a target
XX CC cell-specific portion, comprising an humanised monoclonal antibody,
XX CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX CC binding fragment and a cytotoxic portion having endonucleolytic activity,
XX CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
XX CC compound has cytostatic activity useful for treating cancer and acting as
XX CC a potential inducer of apoptosis.
XX SQ Sequence 517 AA;

Query Match 99.6%; Score 1362; DB 22; Length 517;
Best Local Similarity 99.6%; Pred. No. 3.2e-146;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 60
DB 258 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 317

QY 61 DTYHYVSEPLGRKSYKERYLFVYRPDOVSADVSYVDGCGPCGNDTFNREPAIVRFFS 120
DB 318 DTYHYVSEPLGRKSYKERYLFVYRPDOVSADVSYVDGCGPCGNDTFNREPAIVRFFS 377

QY 121 RFEVREPAIVPLHAAPGDVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
DB 378 RFEVREPAIVPLHAAPGDVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 437

QY 181 WSSIRLWTSPTFQWLIIPDSADTTATPTHCAYDRIVVAGMLLRGAVVDPDSALPFNFQAYG 240
DB 438 WSSIRLWTSPTFQWLIIPDSADTTATPTHCAYDRIVVAGMLLRGAVVDPDSALPFNFQAYG 497

QY 241 LSDQLAQAIISDHPYVEVWLK 260
DB 498 LSDQLAQAIISDHPYVEVWLK 517

RESULT 12
AAM52164
ID AAM52164 standard; Protein; 519 AA.
XX AC AAM52164;
XX AC AAM52164;
DT 05-FEB-2002 (first entry)
XX DE Humanised HMFG-1 Fd/DNase I fusion protein 4.
XX KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
XX KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200174905-A1.

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XX PD 11-OCT-2001.
XX PF 26-MAR-2001; 2001WO-GB01324.
XX PR 03-APR-2000; 2000GB-0008049.
XX PR 02-OCT-2000; 2000US-237159P.
XX PA (ANTI-) ANTISOMA RES LTD.
XX PI Young RJ;
XX PI WPI; 2001-662969/76.
XX DR Novel compound used to treat cancer has target cell-specific portion
XX PT comprising humanised monoclonal antibody having specificity for
XX PT polymorphic epithelial mucin, and cytotoxic portion having
XX PT endonucleolytic activity -
XX XX
XX PS Claim 20; Figure 15; 176pp; English.
XX CC The invention relates to a compound which comprises a target
XX CC cell-specific portion, comprising an humanised monoclonal antibody,
XX CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX CC binding fragment and a cytotoxic portion having endonucleolytic activity,
XX CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
XX CC compound has cytostatic activity useful for treating cancer and acting as
XX CC a potential inducer of apoptosis.
XX SQ Sequence 519 AA;

Query Match 99.6%; Score 1362; DB 22; Length 519;
Best Local Similarity 99.6%; Pred. No. 3.2e-146;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGGETKMSNATLSYIVQILSRVDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
DB 260 LKIAAFNIQTGGETKMSNATLSYIVQILSRVDIALVQEVDRSHLTAVGKLLDNLNQDAP 319
QY 61 DTYHYVVSSEPLGRKSYKERYLFVYRDPQVSAVDVSYDDGCGPCGNDTFNREPAIVRPF 120
DB 320 DTYHYVVSSEPLGRKSYKERYLFVYRDPQVSAVDVSYDDGCGPCGNDTFNREPAIVRPF 379
QY 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMLMGDFNAGCSYVRPSQ 180
DB 380 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMLMGDFNAGCSYVRPSQ 439
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPPDSALPFFNQAAAYG 240
DB 440 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPPDSALPFFNQAAAYG 499
QY 241 LSDQLAQAIISDHYFVEMVK 260
DB 500 LSDQLAQAIISDHYFVEMVK 519

RESULT 13
AAM52163
ID AAM52163 standard; Protein; 521 AA.
XX AC AAM52163;
XX XX
XX DT 05-FEB-2002 (first entry)
XX DE Humanised HMFG-1 Fd/DNase I fusion protein 3.
XX KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
XX KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200174905-A1.

XX PD 11-OCT-2001.
XX PF 26-MAR-2001; 2001WO-GB01324.
XX PR 03-APR-2000; 2000GB-0008049.
XX PR 02-OCT-2000; 2000US-237159P.
XX PA (ANTI-) ANTISOMA RES LTD.
XX PI Young RJ;
XX PI WPI; 2001-662969/76.
XX DR Novel compound used to treat cancer has target cell-specific portion
XX PT comprising humanised monoclonal antibody having specificity for
XX PT polymorphic epithelial mucin, and cytotoxic portion having
XX PT endonucleolytic activity -
XX XX
XX PS Claim 20; Figure 14; 176pp; English.
XX CC The invention relates to a compound which comprises a target
XX CC cell-specific portion, comprising an humanised monoclonal antibody,
XX CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX CC binding fragment and a cytotoxic portion having endonucleolytic activity,
XX CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
XX CC compound has cytostatic activity useful for treating cancer and acting as
XX CC a potential inducer of apoptosis.
XX SQ Sequence 521 AA;

Query Match 99.6%; Score 1362; DB 22; Length 521;
Best Local Similarity 99.6%; Pred. No. 3.2e-146;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGGETKMSNATLSYIVQILSRVDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
DB 262 LKIAAFNIQTGGETKMSNATLSYIVQILSRVDIALVQEVDRSHLTAVGKLLDNLNQDAP 321
QY 61 DTYHYVVSSEPLGRKSYKERYLFVYRDPQVSAVDVSYDDGCGPCGNDTFNREPAIVRPF 120
DB 322 DTYHYVVSSEPLGRKSYKERYLFVYRDPQVSAVDVSYDDGCGPCGNDTFNREPAIVRPF 381
QY 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMLMGDFNAGCSYVRPSQ 180
DB 382 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMLMGDFNAGCSYVRPSQ 441
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPPDSALPFFNQAAAYG 240
DB 442 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPPDSALPFFNQAAAYG 501
QY 241 LSDQLAQAIISDHYFVEMVK 260
DB 502 LSDQLAQAIISDHYFVEMVK 521

RESULT 14
AAM52166
ID AAM52166 standard; Protein; 525 AA.
XX AC AAM52166;
XX XX
XX DT 05-FEB-2002 (first entry)
XX DE Humanised HMFG-1 Fd/DNase I fusion protein 6.
XX KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
XX KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200174905-A1.

XX PD 11-OCT-2001.
 XX PF 26-MAR-2001; 2001WO-GB01324.
 XX PR 03-APR-2000; 2000GB-0008049.
 XX PR 02-OCT-2000; 2000US-237159P.
 XX PA (ANTI-) ANTISOMA RES LTD.
 XX PI Young RJ;
 XX PI WPI; 2001-662969/76.
 XX Novel compound used to treat cancer has target cell-specific portion
 PT comprising humanised monoclonal antibody having specificity for
 PT polymorphic epithelial mucin, and cytotoxic portion having
 PT endonucleolytic activity -
 XX Claim 20; Figure 17; 176pp; English.
 XX The invention relates to a compound which comprises a target
 CC cell-specific portion, comprising an humanised monoclonal antibody,
 CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis.
 XX Sequence 525 AA;

Query Match 99.6%; Score 1362; DB 22; Length 525;
 Best Local Similarity 99.6%; Pred. No. 3.3e-146;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKIAAFNIQTGETKMSNATLVSVIVQILSRDYALVQEVDRDHLTAVGKLLDNLNDAP 60
 Db 256 LKIAAFNIQTGETKMSNATLVSVIVQILSRDYALVQEVDRDHLTAVGKLLDNLNDAP 315

Qy 61 DTHYVYVSEPLGRKSYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNREPAIVRFS 120
 Db 316 DTHYVYVSEPLGRKSYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNREPAIVRFS 375

Qy 121 RFEVREFAIVPLHAAFGDAVAEIDALYDVLVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
 Db 376 RFEVREFAIVPLHAAFGDAVAEIDALYDVLVQEKWGLEDMVLMGDFNAGCSYVRPSQ 435

Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAAYG 240
 Db 436 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAAYG 495

Qy 241 LSDQLAQAI SDHYFVEMLK 260
 Db 496 LSDQLAQAI SDHYFVEMLK 515

RESULT 15
 AAM52155
 ID AAM52155 standard; Protein; 527 AA.
 XX AC AAM52155;
 XX DT 05-FEB-2002 (first entry)
 XX DE Humanised HMFG-1 Fd/DNase I/SV40 NLS fusion protein.
 XX KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
 XX KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
 XX OS Chimeric - Homo sapiens.
 XX OS Chimeric - Rhesus macaque polyoma virus.
 XX OS Synthetic.

PN WO200174905-A1.
 XX PD 11-OCT-2001.
 XX PF 26-MAR-2001; 2001WO-GB01324.
 XX PR 03-APR-2000; 2000GB-0008049.
 XX PR 02-OCT-2000; 2000US-237159P.
 XX PA (ANTI-) ANTISOMA RES LTD.
 XX PI Young RJ;
 XX PI WPI; 2001-662969/76.
 XX Novel compound used to treat cancer has target cell-specific portion
 PT comprising humanised monoclonal antibody having specificity for
 PT polymorphic epithelial mucin, and cytotoxic portion having
 PT endonucleolytic activity -
 XX Claim 20; Figure 6; 176pp; English.
 XX The invention relates to a compound which comprises a target
 CC cell-specific portion, comprising an humanised monoclonal antibody,
 CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis.
 XX Sequence 527 AA;

Query Match 99.6%; Score 1362; DB 22; Length 527;
 Best Local Similarity 99.6%; Pred. No. 3.3e-146;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKIAAFNIQTGETKMSNATLVSVIVQILSRDYALVQEVDRDHLTAVGKLLDNLNDAP 60
 Db 258 LKIAAFNIQTGETKMSNATLVSVIVQILSRDYALVQEVDRDHLTAVGKLLDNLNDAP 317

Qy 61 DTHYVYVSEPLGRKSYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNREPAIVRFS 120
 Db 318 DTHYVYVSEPLGRKSYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNREPAIVRFS 377

Qy 121 RFEVREFAIVPLHAAFGDAVAEIDALYDVLVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
 Db 378 RFEVREFAIVPLHAAFGDAVAEIDALYDVLVQEKWGLEDMVLMGDFNAGCSYVRPSQ 437

Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAAYG 240
 Db 438 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAAYG 497

Qy 241 LSDQLAQAI SDHYFVEMLK 260
 Db 498 LSDQLAQAI SDHYFVEMLK 517

Search completed: November 21, 2003, 13:55:10
 Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 13:46:05 ; Search time 21 Seconds
(without alignments)
1190.660 Million cell updates/sec

Title: US-10-005-306-9
Perfect score: 1367
Sequence: 1 LKIAAFNIQTGTGKMSNAT.....LSQLAQAISDHPVEVMLK 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	99.6	282	1 NDHUI	deoxyribonuclease
2	1129	82.6	284	1 S13676	deoxyribonuclease
3	1127	82.4	284	1 J23526	deoxyribonuclease
4	1072	78.4	262	1 A36324	deoxyribonuclease
5	1067	78.1	282	1 NDHUI	deoxyribonuclease
6	1061	77.6	260	1 B26325	deoxyribonuclease
7	591	43.2	302	2 J23561	deoxyribonuclease
8	464.5	34.0	302	2 J23561	deoxyribonuclease
9	128	9.4	1067	2 D75625	probable extracellular
10	100.5	7.4	1646	1 WMTS2	18k protein - cuc
11	94	6.9	1070	2 T31332	nuclease - Aeronon
12	93.5	6.8	2163	2 S06675	pre-mRNA splicing
13	91	6.7	488	2 T1160	hypothetical prote
14	91	6.7	761	2 A81848	hypothetical prote
15	90	6.6	337	2 G82453	lipase, GDXG fami
16	88.5	6.5	534	2 AB0392	probable carboxydr
17	88	6.4	929	2 T17392	vrli protein - Dic
18	87	6.4	441	2 H66817	hypothetical prote
19	87	6.4	779	2 E83157	hypothetical prote
20	87	6.4	831	2 T05265	coat protein gamma
21	86.5	6.3	299	2 H82845	2,3,4,5-tetrahydro
22	85.5	6.3	916	2 J70396	reverse transcript
23	85.5	6.3	991	2 A99334	hypothetical prote
24	84	6.1	267	2 S38044	hypothetical prote
25	84	6.1	394	2 F90598	membrane nuclease
26	83.5	6.1	345	2 T48351	adenosine kinase-1
27	83.5	6.1	1102	2 T02782	probable relaxase
28	83	6.1	742	2 E83061	probable TonB-depe
29	82	6.0	403	2 T17501	major capsid-like

ALIGNMENTS

RESULT 1

NDHUI

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 08-Dec-2000

C:Accession: A38417; E00036; PS0144

R:Shak, S.; Capon, D.J.; Hellmiss, R.; Marsters, S.A.; Baker, C.L.

Proc. Natl. Acad. Sci. U.S.A. 87, 9188-9192, 1990

A:Title: Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum.

A:Reference number: A38417; NUID:91067672; PMID:2251263

A:Accession: A38417

A:Molecule type: mRNA

A:Residues: 1-282 <SHA>

A:Cross-references: GB:M55983; MID:g181623; PIDN:AA63170.1; PID:g181624

R:Rosenstreich, D.L.; Tu, J.H.; Kinkade, F.R.; Maurer-Fogy, I.; Kahn, J.; Barton, R.W.

J. Exp. Med. 168, 1767-1779, 1988

A:Title: A human urine-derived interleukin 1 inhibitor. Homology with deoxyribonuclease

A:Reference number: E00036; MUID:89035996; PMID:3263467

A:Accession: E00036

A:Molecule type: protein

A:Residues: 23-25, 'X', 27-30, 'X', 32-39, 'X', 41-43, 'X', 45, 73-95 <ROS>

R:Yasuda, T.; Awazu, S.; Sato, W.; Iida, R.; Tanaka, Y.; Kishi, K.

J. Biochem. 108, 393-398, 1990

A:Title: Human genetically polymorphic deoxyribonuclease: purification, characterization

A:Reference number: PS0144; MUID:91115785; PMID:2277032

A:Accession: PS0144

A:Molecule type: protein

A:Residues: 23-39, 'X', 41-49 <YAS>

C:Genetics:

A:Gene: GDB:DNASE1; DNLI

A:Cross-references: GDB:132846; OMIM:125505

A:Map position: 16p13.3-16p13.3

C:Superfamily: deoxyribonuclease I

C:Keywords: glycoprotein, hydrolase

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-282/Product: deoxyribonuclease I #status experimental <NAT>

F:40,128/Binding site: carboxylate (Asn) (covalent) #status predicted

F:156/Active site: His #status predicted

Query Match 99.6%; Score 1362; DB 1; Length 282;
Best Local Similarity 99.6%; Pred. No. 1.1e-117;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKIAAFNIQTGTGKMSNATLSVYVQLSRDYIALVQVDRSHLTAVGKLLDNLNADP 60

Db 23 LKIAAFNIQTGTGKMSNATLSVYVQLSRDYIALVQVDRSHLTAVGKLLDNLNADP 82

Qy 61 DTHYVVSSEPLGCKSKYKRYLFVYVPDQVSAVDSVYDDGCGPCGNDPNEPAIVRFFS 120

Db 83 DTHYVVSSEPLGCKSKYKRYLFVYVPDQVSAVDSVYDDGCGPCGNDPNEPAIVRFFS 142

Qy 121 RFTVEVFAIVPLHAAPGDAVAIEDALYDVYLDVQEKNGLEDVLMGDFNAGCSYVRPSQ 180

L2 protein - human
membrane nuclease
annexin IV - pig
probable D-lactate
genome polyprotein
annexin IV - bovin
phosphoglycerate t
acid phosphatase t
subtilisin-like pr
aerobactin biosynt
protein T24E12.10
hypothetical prote
exodeoxyribonuclea
hypothetical prote
two-component hybr
conserved hypothet

30 82 5.0 470 1 P2WL39
31 81.5 6.0 434 2 C82885
32 81 5.9 318 1 LURGA
33 80.5 5.9 473 2 H72744
34 80.5 5.9 2157 1 GNNY1B
35 80 5.9 319 1 LUBO4
36 80 5.9 439 2 R82426
37 80 5.9 467 2 S3476
38 79.5 5.8 478 1 S61986
39 79.5 5.8 580 2 T44481
40 79.5 5.8 632 2 G88109
41 79.5 5.8 723 2 H90481
42 79 5.8 269 2 G71673
43 79 5.8 497 2 T48367
44 79 5.8 1299 2 RH2090
45 78.5 5.7 387 2 AD0890

Db 143 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMDFNAGCSYVRPSQ 202
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDPSALPQAAAYG 240
Db 203 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDPSALPQAAAYG 262
QY 241 LSDQLAQAIISDHYFVPEVMLK 260
Db 263 LSDQLAQAIISDHYFVPEVMLK 282

RESULT 2

S13676
deoxyribonuclease I (EC 3.1.21.1) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S13676
R:Polzar, B.; Mannherz, H.G.
Nucleic Acids Res. 18, 7151, 1990
A:Title: Nucleotide sequence of a full length cDNA clone encoding the deoxyribonuclease
A:Reference number: S13676; MUID:91088312; PMID:2263485
A:Accession: S13676
A:Molecule type: mRNA
A:Residues: 1-284 <POL>
A:Cross-references: EMBL:X56060
C:Superfamily: deoxyribonuclease I
C:Keywords: hydrolase

Query Match 82.6%; Score 1129; DB 1; Length 284;
Best Local Similarity 80.4%; Pred. No. 3e-96;
Matches 209; Conservative 29; Mismatches 22; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGETKMSNATLSVYIQLSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
Db 23 LRIAAPNIRTFGETKMSNATLSVYIQLSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 82
QY 61 DTYHYVSEPLGRKSKYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNRPAPVRFPS 120
Db 83 DNYRIISPEPLGRKSKYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNRPAPVRFPS 142
QY 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
Db 143 PYTEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMDFNAGCSYVRPSQ 202
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDPSALPQAAAYG 240
Db 203 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDPSALPQAAAYG 262
QY 241 LSDQLAQAIISDHYFVPEVMLK 260
Db 263 LTNQMAEAIISDHYFVPEVTLR 282

RESULT 3

JC2526
deoxyribonuclease I (EC 3.1.21.1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JC2526
R:Feitsch, M.C.; Imler, M.; French, L.E.; Tschoopp, J.
Biochem. Biophys. Res. Commun. 207, 62-68, 1995
A:Title: Genomic organisation and expression of mouse deoxyribonuclease I.
A:Reference number: JC2526; MUID:95160718; PMID:7857306
A:Accession: JC2526
A:Molecule type: mRNA
A:Residues: 1-284 <PEI>
A:Cross-references: EMBL:U00478; NID:G437052; PIDN:AAA03710.1; PID:G437053
C:Superfamily: deoxyribonuclease I
C:Keywords: actin binding; calcium binding; hydrolase

Query Match 82.4%; Score 1127; DB 1; Length 284;
Best Local Similarity 81.5%; Pred. No. 4.6e-96;

Matches 212; Conservative 23; Mismatches 25; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGETKMSNATLSVYIQLSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
Db 23 LRIAAPNIRTFGETKMSNATLSVYIQLSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 82
QY 61 DTYHYVSEPLGRKSKYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNRPAPVRFPS 120
Db 83 DTYHYVSEPLGRKSKYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNRPAPVRFPS 142
QY 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
Db 143 PYTEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMDFNAGCSYVRPSQ 202
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDPSALPQAAAYG 240
Db 203 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDPSALPQAAAYG 262
QY 241 LSDQLAQAIISDHYFVPEVMLK 260
Db 263 LSNQMAEAIISDHYFVPEVTLR 282

RESULT 4

A26324
deoxyribonuclease I (EC 3.1.21.1) - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26324
R:Paudel, H.K.; Liao, T.H.
J. Biol. Chem. 261, 16006-16011, 1986
A:Title: Purification, characterization, and the complete amino acid sequence of porcine
A:Reference number: A26324; MUID:87057260; PMID:3782104
A:Accession: A26324
A:Molecule type: protein
A:Residues: 1-262 <PAU>
C:Superfamily: deoxyribonuclease I
C:Keywords: hydrolase

Query Match 78.4%; Score 1072; DB 1; Length 262;
Best Local Similarity 77.3%; Pred. No. 4.8e-91;
Matches 201; Conservative 30; Mismatches 29; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLSVYIQLSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
Db 1 LKIAAFNIRTFGETKMSNATLSVYIQLSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
QY 61 DTYHYVSEPLGRKSKYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNRPAPVRFPS 120
Db 61 NNYHHVSEPLGRKSKYKERYLFVYRPDQVSAVDYDDGCEPCGNDTFNRPAPVRFPS 120
QY 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
Db 121 PFTQVKEFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDPSALPQAAAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDPSALPQAAAYG 240
QY 241 LSDQLAQAIISDHYFVPEVMLK 260
Db 241 LSQETALAIISDHYFVPEVTLK 260

RESULT 5

NDBOA
deoxyribonuclease I (EC 3.1.21.1) precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jun-2000
C:Accession: JG6552; A92123; A92148; A26325; A00782; S19525
R:Chen, C.Y.; Lu, S.C.; Liao, T.H.
Gene 206, 181-184, 1998
A:Title: Cloning, sequencing and expression of a cDNA encoding bovine pancreatic deoxy

A:Reference number: JC6532; MUID:98137790; PMID:9469931
A:Accession: JC6532
A:Molecule type: mRNA
A:Residues: 1-282 <CHE>
A:Cross-references: GB:AJ001538; MID:92546887; PIDN:CAA04819.1; PID:92546888
R:Liao, T.H.; Sainikow, J.; Moore, S.; Stein, W.H.
J. Biol. Chem. 248, 1489-1495, 1973
A:Title: Bovine pancreatic deoxyribonuclease A. Isolation of cyanogen bromide peptides:
A:Reference number: A92123; MUID:73097126; PMID:4734471
A:Accession: A92123
A:Molecule type: protein
A:Residues: 23-49,53-59, 'EQ', 62-248, 'GP', 251-282 <LI1>
A:Experimental source: deoxyribonuclease A
A:Note: this sequence revised in reference A89338
A:Note: disulfide bonds link residues 123-126 and 195-231; the former bond can be reduced
R:Liao, T.H.; Sainikow, J.; Moore, S.; Stein, W.H.
J. Biol. Chem. 267, 7957, 1992
A:Reference number: A38938; MUID:92218466; PMID:1348510
A:Contents: annotation; revisions
R:Sainikow, J.; Murphy, D.
J. Biol. Chem. 248, 1499-1501, 1973
A:Title: Bovine pancreatic deoxyribonucleases A and C. A proline for histidine substitution
A:Reference number: A92124; MUID:73149229; PMID:4735117
A:Accession: A92124
A:Molecule type: protein
A:Residues: 23-49,53-59, 'EQ', 62-142, 'P', 144-248, 'GP', 251-282 <SAL>
A:Experimental source: deoxyribonuclease C
R:Liao, T.H.
J. Biol. Chem. 249, 2354-2356, 1974
A:Title: Bovine pancreatic deoxyribonuclease D.
A:Reference number: A92148; MUID:74143471; PMID:4856650
A:Accession: A92148
A:Molecule type: protein
A:Residues: 23-49,53-59, 'EQ', 62-142, 'P', 144-248, 'GP', 251-282 <LI2>
A:Experimental source: deoxyribonuclease D
A:Note: the C and D forms differ from the A and B forms in having 143-Pro; the only difference bound to Asp-40
R:Paudel, H.K.; Liao, T.H.
J. Biol. Chem. 261, 16012-16017, 1986
A:Title: Comparison of the three primary structures of deoxyribonuclease isolated from B. ovis, B. taurus, and B. melandryi.
A:Reference number: A26325; MUID:87057261; PMID:3782105
A:Accession: A26325
A:Molecule type: protein
A:Residues: 39, 'X', 41-58 <PAU>
R:Price, P.A.; Moore, S.; Stein, W.H.
J. Biol. Chem. 244, 924-928, 1969
A:Title: Alkylation of a histidine residue at the active site of bovine pancreatic deoxyribonuclease.
A:Reference number: A92054; MUID:69184134; PMID:4976790
A:Contents: annotation
A:Note: in the presence of divalent cations, His-156 is alkylated by iodoacetate with covalent modification
R:Hugli, T.E.; Stein, W.H.
J. Biol. Chem. 246, 7191-7200, 1971
A:Title: Involvement of a tyrosine residue in the activity of bovine pancreatic deoxyribonuclease.
A:Reference number: A92094; MUID:72064723; PMID:5166750
A:Contents: annotation
A:Note: nitration of Tyr-87 by tetranitromethane destroys a calcium binding site and inactivates the enzyme
R:Lamm, A.; Suck, D.
J. Mol. Biol. 221, 645-667, 1991
A:Title: DNase I-induced DNA conformation. 2 A structure of a DNase I-octamer complex.
A:Reference number: S19525
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
A:Function:
A:Description: catalyzes the hydrolysis of DNA to 5'-phosphodinucleotides and 5'-phosphodiphosphates
C:Superfamily: deoxyribonuclease I
C:Keywords: glycoprotein; hydrolase; nucleic acid degradation
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-282/Product: deoxyribonuclease I #status experimental <MAT>
F:40/Binding site: carboxylate (Asn) (covalent) #status experimental
F:123-126,195-231/Disulfide bonds: #status experimental

Query Match 78.1%; Score 1067; DB 1; Length 282;
Best Local Similarity 78.0%; Pred. No. 1.5e-90;

Matches 202; Conservative 28; Mismatches 29; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGETKSNATLVSYVQILSRVDIALVQVRDLSHLTAVGKLLDNLNQDAP 60
DB 23 LKIAAFNIQTGETKSNATLVSYVQILSRVDIALVQVRDLSHLTAVGKLLDNLNQDAP 60
QY 61 DTYHYVVSSEPLGRKSKERYLFFVRPDQVSAVDYDDGCEPCGNDTFNREPAIVRFS 120
DB 83 NYHYVVSSEPLGRKSKERYLFFVRPDQVSAVDYDDGCEPCGNDTFNREPAIVRFS 142
QY 121 RFTVEVREPAIVPLHAAPGDAVAEIDALVDYVQVKGLDVMGMGDFNAGCSYVRPSQ 180
DB 143 HSTKVKFAIVLHSGAPSDAFAEINSLYDVLQVQKWLNDVWMLMGDFNADCSYVTSQ 202
QY 181 WSSIRLWTSPTQWLIPDSADTTATPHCAVDRIIVAGMLRGAVVPDSALPFPQAAVG 240
DB 203 WSSIRLWTSPTQWLIPDSADTTATPHCAVDRIIVAGMLRGAVVPDSALPFPQAAVG 262
QY 241 LSDQLAQAISSDHPYVEVTL 259
DB 263 LSNEWALAISSDHPYVEVTL 281
RESULT 6
B26325
deoxyribonuclease I (EC 3.1.21.1) - sheep
C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: B26325
R:Paudel, H.K.; Liao, T.H.
J. Biol. Chem. 261, 16012-16017, 1986
A:Title: Comparison of the three primary structures of deoxyribonuclease isolated from B. ovis, B. taurus, and B. melandryi.
A:Reference number: A26325; MUID:87057261; PMID:3782105
A:Accession: B26325
A:Molecule type: protein
A:Residues: 1-260 <PAU>
C:Superfamily: deoxyribonuclease I
C:Keywords: hydrolase
Query Match 77.6%; Score 1061; DB 1; Length 260;
Best Local Similarity 77.2%; Pred. No. 4.9e-90;
Matches 200; Conservative 32; Mismatches 27; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGETKSNATLVSYVQILSRVDIALVQVRDLSHLTAVGKLLDNLNQDAP 60
DB 1 LKIAAFNIQTGETKSNATLVSYVQILSRVDIALVQVRDLSHLTAVGKLLDNLNQDAP 60
QY 61 DTYHYVVSSEPLGRKSKERYLFFVRPDQVSAVDYDDGCEPCGNDTFNREPAIVRFS 120
DB 61 NSHYVVSSEPLGRKSKERYLFFVRPDQVSAVDYDDGCEPCGNDTFNREPAIVRFS 120
QY 121 RFTVEVREPAIVPLHAAPGDAVAEIDALVDYVQVKGLDVMGMGDFNAGCSYVRPSQ 180
DB 121 PSTKYKFAIVLHSGAPSDAFAEINSLYDVLQVQKWLNDVWMLMGDFNADCSYVTSQ 180
QY 181 WSSIRLWTSPTQWLIPDSADTTATPHCAVDRIIVAGMLRGAVVPDSALPFPQAAVG 240
DB 181 WSSIRLWTSPTQWLIPDSADTTATPHCAVDRIIVAGMLRGAVVPDSALPFPQAAVG 240
QY 241 LSDQLAQAISSDHPYVEVTL 259
DB 241 LSNEWALAISSDHPYVEVTL 259
RESULT 7
JC5361
deoxyribonuclease I (EC 3.1.21.1) precursor - human
N:Alternate names: DNase; thymonuclease
C:Species: Homo sapiens (man)
C>Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 07-May-1999
C:Accession: JC5361
R:Zeng, Z.; Parmelee, D.; Hyaw, H.; Coleman, T.A.; Su, K.; Zhang, J.; Gentz, R.; Ruben

A;Accession: JQ1157
A;Molecule type: genomic RNA
A;Residues: 1-1646 <UGA>
A;Cross-references: GB:D12505
C;Superfamily: cucumber mosaic

Query Match	7.4%;	Score 100.5;	DB 1;	Length 1646;
Best Local Similarity	22.9%;	Pred. No. 1.5;		
Matches 56;	Conservative 37;	Mismatches 81;	Indels 71;	Gaps 14;
Qy	46	TAVGKLIDNLNQAP--DTY-HYVWSEPLGR-----KSYKERYLFVYRPDQVSA-----91		
Db	1311	SAVGQLANFNFDLPAPFDITTMHMIKRQPKSKRLDTSIQSEYPALQTIYVHKVNVAVGPGV 1370		
Qy	92	-----VDS-----YYVDDCEPCGNDTFNREPAIVRFRFRFEVREFAIVPLHAAP 137		
Db	1371	FKYLTTKFLSNVDSKFFFY-----TRKKPEDLQEFFSGLDSHSDYEILELDVSK 1420		
Qy	138	GDVAEIDALDYVLVDYQEWGLGEDVW-----LMGDFNAGCS-----YVRPSQWS 182		
Db	1421	YDK-QSQSDFFHSIEMAIWEKGLDLDILANWMSGHKRTILQDFQAGIKTLIYYQRKS--G 1477		
Qy	183	SIRLWSPTF-----QWLIPDSADTTATTHCAYDAIVVAGMLRCANVPD-----SALP 232		
Db	1478	DVTTFTGNTFTIIAACVASMPLP-LDKCFKASFCDGDSLI---YLPKGEYEPDIQATANLV 1532		
Qy	233	FNFAQ 237		
Db	1533	WNFEA 1537		

```

RESULT 11
T31332
nuclease - Aeromonas hydrophila
C:Species: Aeromonas hydrophila
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T31332
R;Dodd, H.N.; Pemberton, J.M.
J. Bacteriol. 178, 3926-3933, 1996
A>Title: Cloning, sequencing, and characterization of the nuch gene encoding an
A:Reference number: Z20999; MUID:96272269; PMID:8682799
A:Accession: T31332
A:Status: preliminary; translated from GE/EMBL/DDDBJ
A:Molecule type: DNA
A:Residues: 1-1070 <DOD>
A:Cross-references: EMBL:L76304; NID:g1185048; PID:g1185049; PIDN:AAB39273.1
C:Genetics:
A:Gene: nuch

```

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Query Match      6.9%; Score 94; DB 2; Length 1070;
Best Local Similarity 20.7%; Pred. No. 3.4;
Matches 63; Conservative 39; Mismatches 90; Indels 114; Gaps 14;

QY      1  LKTAARNIQTF-----GETKMSNATLVSYIVQILSRVDIALVQE 39
      ||:||:||:||||:||||:||||:||||:||||:||||:||||:
Db      477  LRVASFNVLNFFTTVVGGDANPTNSNRGALTGVGEFQRTKIIVSAITRL--NADVVGVLME 534

QY      40  VRDS-----HLTAVGKLLDNLNODAPDTVHYVVSPELGRKSYKERYLFWRPDQVSAVDYY 96
      ||:||:||:||||:||||:||||:||||:||||:||||:
Db      535  IEDNGYNNISAITANLVGALNALPDE-----QDHYAFVHSPDD----- 572

QY      97  YDDGCPGCGNDTFN----REPATVRFPSRFTVEFEA--IVPLHAAPGDAVAEIDALYDV 150
      ||:||:||:||||:||||:||||:||||:||||:||||:
Db      573  -----QPMGTGDAITVGLIYRPKAVSL-----EGAAQLIPLPLQVAEAVDQADK-- 615

QY      151  YLDVQEKWGLELDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFOWLI----- 196
      ||:||:||:||||:||||:||||:||||:||||:||||:
Db      616  --PVSIRQWRD-----SLLQRTSPKGDVPLTVVNHLLKKSAC 654

QY      197  ----PD--SADTTATPTHCAIDRIVVAGML--LRGAVVPSGALPFNFQAAVGLSDQLAQAI 249
      ||:||:||:||||:||||:||||:||||:||||:||||:
Db      655  YEDYPDYVTDADPLDGGQHCNALRVSAAKVLGEISLKOEPGDLLVIGDNLNAGLEDPV--RVL 713
      ||:||:||:||||:||||:||||:||||:||||:||||:

```

Qy	250	SDHP	254
	:	:	:
Db	714	TDYP	718
RESULT 12			
pre-mRNA splicing helices			
N;Alternate names: DNA 1			
C;Species: Saccharomyces			
C;Date: 28-May-1993 #se			
C;Accession: S50675; S3			
R;Dietrich, F.S.			
submitted to the EMBL Data			
A;Description: The sequen			
A;Reference number: S50			
A;Accession: S50675			
A;Molecule type: DNA			
A;Residues: 1-2163 <DIE			
A;Cross-references: EMB			
R;Mulligan, J.T.; Dietri			
submitted to the EMBL Data			
A;Reference number: S30			
A;Accession: S30856			
A;Molecule type: DNA			
A;Residues: 1-169 <MUL			
A;Cross-references: EMB			
R;Zhu, Y.B.; Prakash, L			
Chinese Biochem J 11,			
A;Title: Molecular clon			
A;Reference number: JC4			
A;Accession: JC4657			
A;Molecule type: DNA			
A;Residues: 1-260,'HCQT			
C;Genes:			
A;Gene: SGD:BRR2; RAD24			
A;Cross-references: SGD			
A;Map position: 5R			
C;Keywords: ATP; DNA rep			
F;521-528/Region: nucle			
F;630-635/Region: nucle			
F;634-637/Region: DEXH			

Query Match	6.8%;	Score 93.5;	DB 2;	Length 2163;	
Best Local Similarity	24.8%;	Pred. No. 9.5;			
Matches	69;	Conservative 30;	Mismatches 86;	Indels 93;	Gaps 16;
QY	10	TEGSE---	TKMSNATLVSIVIOILRSYDIALVQEVDRDLSHTAVGKLLDLNL	-----	56
DB	882	TFGBGIIITDQSN--	VQYLSVLNQ-----QLPIESQF--VSKLVLDNLNAE	VAGNIK	930
QY	57	--QDAPD-----	TYHYV--VSEPLGK-----SYKERYLVFV-	84	
DB	931	CRNDANVWLAYLYLYVRLASPLVYDPDISDGO	LKKFRESLVHSALCILEQELVLVD	990	
QY	85	RPDQVSAVD-----	SYYYDDGCEPCGNDTRENRE-----PAIVRFFS-	120	
DB	991	AENDVIEATDIGNIASSFYINH- ---	ASMDVYNRELDSEHTTQIDLFRIFSMSEEFKYVSV	1046	
QY	121	RTEVREF-----	AIIVPHAAPGDAVEIDALYDVYLDVQ--EKWGLIEDVLMGDFNAG	172	
DB	1047	RYEEKRELKLEKAPIREDIDIDPLAKVNVLLQSYFSQLK	FEFALNSDIVFTHQVAG	1106	
QY	173	CSYVRPSQWSSIRLWTSPTFQWL-IPDSADTATPTHC	209		
DB	1107	RLLRAMFEICLRKGNGHPTRLMLNLCKSGATTKWPTNC	1144		

RESULT 13
T41160
hypothetical protein SPCC18.17c - fission yeast (Schizosaccharomyces pombe)
C1:Species: Schizosaccharomyces pombe
C1:Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 04-Mar-2000

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 13:45:00 ; Search time 17 seconds
(without alignments)
719.232 Million cell updates/sec

Title: US-10-005-306-9

Perfect score: 1367
Sequence: 1 LKIAFNITQTGETKMSNAT.....LSDQLAQAI SDHYVEVWLK 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1362	99.6	282	1	DRNL_HUMAN
2	1139	83.3	284	1	DRNL_MOUSE
3	1139	82.6	284	1	DRNL_RAT
4	1116	81.6	281	1	DRNL_RABIT
5	1072	78.4	262	1	DRNL_PIG
6	1067	78.1	262	1	DRNL_BOVIN
7	1061	77.6	260	1	DRNL_SHEEP
8	762	55.7	282	1	DRNL_CHICK
9	736	53.8	284	1	DRNL_OREMO
10	704.5	51.5	299	1	DRNL_HUMAN
11	601	44.0	310	1	DRNG_MOUSE
12	593	43.4	310	1	DRNG_RAT
13	591	43.2	305	1	DRNG_HUMAN
14	464.5	34.0	302	1	DRNL_HUMAN
15	100.5	7.4	1648	1	RRPO_CGMVS
16	93.5	6.8	2163	1	BR22_YEAST
17	91.5	6.7	456	1	LEU2_STREN
18	87.5	6.4	423	1	SAT_ENTHI
19	85.5	6.3	916	1	RTUK_DROME
20	84	6.1	267	1	YKUE_YEAST
21	84	6.1	318	1	ANX4_RAT
22	83.5	6.1	345	1	ADK3_ARATH
23	83.5	6.1	832	1	POLG_HVIA
24	83.5	6.1	1102	1	TRAA_RHISN
25	82	6.0	470	1	VL2_HPV39
26	81	5.9	318	1	ANX4_PIG
27	80.5	5.9	344	1	ADK1_ARATH
28	80.5	5.9	2157	1	POLG_HVIB
29	80	5.9	318	1	ANX4_BOVIN
30	80	5.9	467	1	PPAB_YEAST
31	80	5.9	874	1	SYV_STRCO
32	79.5	5.8	162	1	Y096_GVCL
33	79.5	5.8	478	1	YSP3_YEAST

34	79	5.8	602	1	IF2P_SULTO
35	78	5.7	1036	1	HPI2_DEIRA
36	78	5.7	1234	1	YKX1_SCHPO
37	77.5	5.7	823	1	DMSA_RHOCA
38	77.5	5.7	901	1	VP3_BTV13
39	77.5	5.7	1430	1	YES3_YEAST
40	76.5	5.6	439	1	PYRC_CHLPE
41	76.5	5.6	445	1	SPGD_SHIBO
42	76.5	5.6	810	1	SC12_ARATH
43	76.5	5.6	899	1	VP3_EHDVA
44	76	5.6	434	1	YSWJ_CAEEL
45	76	5.6	1211	1	ATHL_YEAST

ALIGNMENTS

RESULT 1	DRNL_HUMAN	STANDARD;	PRT;	282 AA.
ID	DRNL_HUMAN			
AC	P24855;			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	01-MAR-1992 (Rel. 21, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Decyribonuclease I precursor (EC 3.1.21.1) (DNase I) (Dornase alfa).			
GN	DNASE1 OR DNLI OR DRN1.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91067652; PubMed=2251263;			
RA	Shak S., Capon D.J., Hellmiss R., Maxsters S.A., Baker C.L.;			
RT	"Recombinant human Dnase I reduces the viscosity of cystic fibrosis sputum.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:9188-9192(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=95283231; PubMed=7762978;			
RA	Yasuda T., Kishi K., Yanagawa Y., Yoshida A.;			
RT	"Structure of the human deoxyribonuclease I (DNase I) gene: identification of the nucleotide substitution that generates its classical genetic polymorphism.";			
RL	Ann. Hum. Genet. 59:1-15(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,			
RA	Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,			
RA	Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S.,			
RA	Ueng S., Tatum O., Campbell C., Fawcett J., Maltbie M., Misra M.,			
RA	Deaven L.;			
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21135483; PubMed=11241278;			
RA	Oliveri M., Daga A., Cantoni C., Lunardi C., Millo R., Puccetti A.;			
RT	"DNase I mediates internucleosomal DNA degradation in human cells undergoing drug-induced apoptosis.";			
RL	Eur. J. Immunol. 31:743-751(2001).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,			
RA	Altshul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Schaefer T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			

Q976al	sulfolobus
P13126	deinococcus
O14116	schizosacch
Q52675	rhodobacter
Q65750	bluetongue
P40061	saccharomyc
O84dk5	chlorobium
P41578	shigella bo
Q9f920	arabidopsis
P33474	epizootic h
O45363	caenorhabdi
P48016	saccharomyc

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Faneley J., Helton E., Kecteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP SEQUENCE OF 23-45 AND 73-95.
RC TISSUE=Urine;
RX MEDLINE=89035996; PubMed=3263467;
RA Rosenstreich D.L., Tu J.H., Kinkade P.R., Maurer-Fogy I., Kahn J.,
RA Barton R.W., Farina P.R.;
RT "A human urine-derived interleukin 1 inhibitor. Homology with
deoxyribonuclease I.";
RL J. Exp. Med. 168:1767-1779 (1988).
RN [7]
RP SEQUENCE OF 23-49.
RC TISSUE=Urine;
RX MEDLINE=91115785; PubMed=2277032;
RA Yasuda T., Awazu S., Sato W., Iida R., Tanaka Y., Kishi K.;
RT "Human genetically polymorphic deoxyribonuclease: purification,
characterization, and multiplicity of urine deoxyribonuclease I.";
RL J. Biochem. 108:393-398 (1990).
RN [8]
RP VARIANT DNASE1*3.
RX MEDLINE=95351715; PubMed=7625762;
RA Yasuda T., Nadano D., Takeshita H., Tenjo E., Kishi K.;
RT "Molecular analysis of the third allele of human deoxyribonuclease I
polymorphism.";
RL Ann. Hum. Genet. 59:139-147 (1995).
RN [9]
RP VARIANT DNASE1*4.
RX MEDLINE=95172237; PubMed=7867802;
RA Yasuda T., Nadano D., Takeshita H., Tenjo E., Sawazaki K., Ootani M.,
RA Kishi K.;
RT "The molecular basis for genetic polymorphism of human
deoxyribonuclease I: identification of the nucleotide substitution
that generates the fourth allele.";
RL FEBS Lett. 359:211-214 (1995).
RN [10]
RP VARIANT DNASE1*5.
RX MEDLINE=98080314; PubMed=9420147;
RA Iida R., Yasuda T., Aoyama M., Tsubota E., Kobayashi M., Yuasa I.,
RA Matsuki T., Kishi K.;
RT "The fifth allele of the human deoxyribonuclease I (DNase I)
polymorphism.";
RL Electrophoresis 18:1936-1939 (1997).
RN [11]
RP VARIANT DNASE1*6.
RX MEDLINE=99310605; PubMed=10381379;
RA Yasuda T., Takeshita H., Iida R., Kogure S., Kishi K.;
RT "A new allele, DNASE1*6, of human deoxyribonuclease I polymorphism
encodes an Arg to Cys substitution responsible for its instability.";
RL Biochem. Biophys. Res. Commun. 260:280-283 (1999).
CC -1- FUNCTION: AMONG OTHER FUNCTIONS, SEEMS TO BE INVOLVED IN CELL
DEATH BY APOPTOSIS. BINDS SPECIFICALLY TO G-ACTIN AND BLOCKS
ACTIN POLYMERIZATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphonucleotide and 5'-phosphogluconucleotide end-products.
CC -1- COFACTOR: DIVALENT CATIONS, PARTICULARLY CALCIUM AND MAGNESIUM.
CC -1- SUBCELLULAR LOCATION: SECRETORY PROTEIN, STORED IN ZYMOGEN
GRANULES AND FOUND IN THE NUCLEAR ENVELOPE.
CC -1- TISSUE SPECIFICITY: PRINCIPALLY IN TISSUES OF THE DIGESTIVE
SYSTEM. HIGHEST LEVELS FOUND IN URINE, BUT ALSO RELATIVELY
ABUNDANT IN SEMEN AND SALIVA.
CC -1- POLYMORPHISM: AT LEAST 6 ALLELES OF DNASE 1 ARE KNOWN: DNASE1*1 TO
DNASE1*6. THE SEQUENCE SHOWN IS THAT OF DNASE1*2.

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-1- DISEASE: DNASE PHENOTYPES HAVE BEEN SHOWN TO BE ASSOCIATED WITH
LIVER DISEASES.

-1- PHARMACEUTICAL: Available under the name Pulmozyme (Genentech).
Used to reduce the viscosity of cystic fibrosis sputum by
hydrolyzing the extracellular DNA released by degenerating
leukocytes that accumulate in response to infection.

-1- SIMILARITY: BELONGS TO THE DNASE I FAMILY.

-1- DATABASE: NAME=Pulmozyme;

NOTES-Clinical information on Pulmozyme;

WWW="http://www.genentech.com/gene/products/information/opportunistic/pulmozyme";

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between the Swiss Institute of Bioinformatics and the EMBL outstation

the European Bioinformatics Institute. There are no restrictions on its

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

EMBL; M55983; AAA63170.1; -;

EMBL; D83195; BAA1841.1; -;

EMBL; AC005203; AAC24721.1; -;

EMBL; AJ298844; CAC12813.1; -;

EMBL; BC029437; AAH29437.1; -;

PIR; A38417; NDHU1.

HSSP; P00639; ZDNI.

DR GEM; HGNC:2956; DNASE1.

MIW; 125505; -;

GO; GO:0005576; C:extracellular; TAS.

InterPro; IPR001582; DNase I.

InterPro; IPR005135; Exo endo phos.

Pfam; PF03372; Exo endo phos_1.

PRINTS; PR00130; DNASEI.

ProDom; PD005408; DNase_I_N; 1.

SMART; SM00476; DNaseIc; 1.

PROSITE; PS00918; DNase_I_2; 1.

PROSITE; PS00919; DNase_I_1; 1.

Hydrolase; Endonuclease; Nuclease; Glycoprotein; Calcium; Signal;

Apoptosis; Actin-binding; Polymorphism; Pharmaceutical.

CHAIN 1 22 DEOXYRIBONUCLEASE I.

DISULFID 123 126 BY SIMILARITY.

DISULFID 195 231 ESSENTIAL FOR ENZYMACTIC ACTIVITY

BY SIMILARITY.

ACT SITE 100 100 BY SIMILARITY.

ACT SITE 156 156 BY SIMILARITY.

CARBOHYD 40 40 N-LINKED (GLCNAC. . .).

CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).

VARIANT 31 31 Q -> E (in allele DNASE1*4).

VARIANT 114 114 FTID=VAR_002264.

VARIANT 154 154 V -> M (in allele DNASE1*5).

VARIANT 207 207 FTID=VAR_009300.

VARIANT 244 244 P -> A (in allele DNASE1*3).

VARIANT 244 244 dBSNP:1799891.

VARIANT 244 244 FTID=VAR_002265.

VARIANT 244 244 R -> C (in allele DNASE1*6).

VARIANT 244 244 FTID=VAR_009301.

VARIANT 244 244 R -> Q (in allele DNASE1*1).

VARIANT 16 16 dBSNP:1053874.

VARIANT 16 16 FTID=VAR_002266.

VARIANT 16 16 L -> H (IN REF. 2).

SEQUENCE 282 AA; 31433 MW; 040042E2D23555B6 CRC64;

Query Match 99.6%; Score 1362; DB 1; Length 282;

Best Local Similarity 99.6%; Pred. No. 1.6e-120;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNQTTCGKSNATLVSVQILSRVDIALVQVSRDLSHTATVSKLLDNLNQAP 60

Db 23 LKIAAFNQTTCGKSNATLVSVQILSRVDIALVQVSRDLSHTATVSKLLDNLNQAP 82

QY 61 DTHYVVSSEPLGRKSKERYLFVVRPDQVSAVDVSYDDGCGCNDTFNREPAIVRPF 120

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Db 83 DTYHYVSEPLGRNSYKERYLFVYRPDQVSAVDYVYDGGCEPCGNDTFNREPAIVRFFS 142
 QY 121 RFEVREFAIPLHAAPGDAVAEIDALYDVYLDVQEKGLDVMGMGDFNAGCSYVRPSQ 180
 Db 143 RFEVREFAIPLHAAPGDAVAEIDALYDVYLDVQEKGLDVMGMGDFNAGCSYVRPSQ 202
 QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLGAIVVPSALPFFNFOAAYG 240
 Db 203 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLGAIVVPSALPFFNFOAAYG 262
 QY 241 LSDQLAQAISSDHPYVEVMLK 260
 Db 263 LSDQLAQAISSDHPYVEVMLK 282

RESULT 2

ID DRN1 MOUSE STANDARD; PRT; 284 AA.

AC P49183; 070532;
 DT 31-FEB-1996 (Rel. 33, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Deoxyribonuclease I precursor (EC 3.1.21.1) (DNase I).
 GN DNASE I OR DNLI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Heart;
 RX MDLINE=95160718; PubMed=7857306;
 RA Peitsch M.C., Imler M., French L.E., Tschoop J.;
 RT "Genomic organization and expression of mouse deoxyribonuclease I";
 RL Biochem. Biophys. Res. Commun. 207:62-68(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Kidney, and Parotid gland;
 RX MDLINE=97335420; PubMed=9192086;
 RA Takeishi H., Yasuda T., Nakajima T., Hosomi O., Nakashima Y.,
 RA Kishi K.;
 RT "Mouse deoxyribonuclease I (DNase I): biochemical and immunological
 characterization, cDNA structure and tissue distribution";
 RL Biochem. Mol. Biol. Int. 42:65-75(1997).
 CC -1- FUNCTION: AMONG OTHER FUNCTIONS, SEEMS TO BE INVOLVED IN CELL
 DEATH BY APOPTOSIS. BINDS SPECIFICALLY TO G-ACTIN AND BLOCKS
 ACTIN POLYMERIZATION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'.
 CC phosphodiesterase and 5'-phosphoguanonucleotide end-products.
 CC -1- COFACTOR: DIVALENT CATIONS, PARTICULARLY CALCIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: SECRETORY PROTEIN, STORED IN ZIMMOGEN
 GRANULES AND FOUND IN THE NUCLEAR ENVELOPE (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: IN STRIATED MUSCLE, KIDNEY, INTESTINE, LIVER,
 LYMPHNODES, BUT NOT IN THE HEART, SPLEEN OR PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
 CC
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 CC
 CC EMBL; U00478; AAA03710.1; -;
 CC EMBL; D83038; BAA28622.1; -;
 CC F01; JC2526; JC2526.
 CC HSP; P00639; 3DNI.
 CC MGP; MG1.103157; Dnasel.
 CC InterPro; IPR001582; DNase I.
 CC InterPro; IPR005135; Exo endo phos.
 CC Pfam; PF03372; Exo_endo_phos; 1.
 CC PRINTS; PR00130; DNASEI.

DR ProDom; PD005408; DNase_I_N; 1.
 DR SMART; SM00476; DNaseIc; 1.
 DR PROSITE; PS00918; DNASE_I_2; 1.
 DR PROSITE; PS00919; DNASE_I_1; 1.
 KW Hydrolase; Endonuclease; Nuclease; Glycoprotein; Calcium; Signal;
 KW Apoptosis; Actin-binding.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 284 DEOXYRIBONUCLEASE I,
 FT DISULFID 123 126 BY SIMILARITY.
 FT DISULFID 195 231 ESSENTIAL FOR ENZYMATIC ACTIVITY
 (BY SIMILARITY).
 FT ACT_SITE 100 100 BY SIMILARITY.
 FT ACT_SITE 156 156 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 239 240 AG -> VR (IN REF. 1).
 SQ SEQUENCE 284 AA; 32027 MW; 8682E20515EEB510 CRC64;

Query Match 83.3%; Score 1139; DB 1; Length 284;
 Best Local Similarity 82.3%; Pred. No. 1.4e-99;
 Matches 214; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 1 LKIAFNITFGTQMSNATLVSYIVQILSRDYIALVQVSRDLSHTAVKGLDNLNODAP 60
 Db 23 LKIAFNITFGTQMSNATLVSYIVQILSRDYIALVQVSRDLSHTAVKGLDNLNODAP 82
 QY 61 DTYHYVSEPLGRNSYKERYLFVYRPDQVSAVDYVYDGGCEPCGNDTFNREPAIVRFFS 120
 Db 83 DTYHYVSEPLGRNSYKERYLFVYRPDQVSAVDYVYDGGCEPCGNDTFNREPAIVRFFS 142
 QY 121 RFEVREFAIPLHAAPGDAVAEIDALYDVYLDVQEKGLDVMGMGDFNAGCSYVRPSQ 180
 Db 143 RFEVREFAIPLHAAPGDAVAEIDALYDVYLDVQEKGLDVMGMGDFNAGCSYVRPSQ 202
 QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLGAIVVPSALPFFNFOAAYG 240
 Db 203 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLGAIVVPSALPFFNFOAAYG 262
 QY 241 LSDQLAQAISSDHPYVEVMLK 260
 Db 263 LSDQLAQAISSDHPYVEVMLK 282

RESULT 3

ID DRN1 RAT STANDARD; PRT; 284 AA.

AC P21704;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Deoxyribonuclease I precursor (EC 3.1.21.1) (DNase I).
 GN DNASE I OR DNLI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Parotid gland;
 RX MEDLINE=91088312; PubMed=2263485;
 RA Polzar B., Manheitz H.G.;
 RT "Nucleotide sequence of a full length cDNA clone encoding the
 deoxyribonuclease I from the rat parotid gland";
 RL Nucleic Acids Res. 18:7151-7151(1990).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=97447693; PubMed=9303433;
 RA Liu Q.Y., Ribocco M., Hou Y., Walker P.R., Sikorska M.;
 RT "DNase I primary transcript is alternatively spliced in both normal
 and apoptotic cells: no evidence of up-regulation in apoptosis";
 RL DNA Cell Biol. 16:911-918(1997).
 [3]

QY 1 LKIAAFNIQTGKTSNATLSYIVQILSRVDIALVOEVRDSDSLTAVGKLLDNLNQDAP 60
 DB 22 LKIAAFNIRSFQETKSNATLSYIVQILSRVDIALVOEVRDSDSLTAVGKLLDNLNEKAA 81
 QY 61 DTYHVVSPELGRKSYKERYLFVVRPDQVSAVDSYVYDDGCEPCGNDTFRPAIVRFFS 120
 DB 82 DTYRVSPELGRKSYKERYLFVVRPDQVSAVDSYVYDDGCEPCGNDTFRPAIVRFFS 141
 QY 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVYDVOEKWGLDVMGMDFNAGCSYVRPSQ 180
 DB 142 PGTKVREFAIVPLHAAPGDAVAEIDALYDVYDVOEKWGLDVMGMDFNAGCSYVRPSQ 201
 QY 181 WSSIRLWTSPTFQWMLIPDSADTTATPTCAVDRIIVVAGMLRGAVVPSALPFRFOAYG 240
 DB 202 WSSIRLWTSPTFQWMLIPDSADTTATPTCAVDRIIVVAGMLRGAVVPSALPFRFOAYG 261
 QY 241 LQDQLAQAISSDHPYVVMK 259
 DB 262 LQDQLAQAISSDHPYVVMK 280

RESULT 5

DRN1_PIG STANDARD; PRT; 262 AA.
 AC P11936;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Deoxyribonuclease I (EC 3.1.21.1) (Dnase I).
 GN DNASE1 OR DNLI.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RC SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RC TISSUE=Pancreas;
 RA MEDLINE=87057260; PubMed=3782104;
 RA Faudel H.K., Liao T.-H.;
 RT "Purification, characterization, and the complete amino acid sequence
 of porcine pancreatic deoxyribonuclease.";
 RL J. Biol. Chem. 261:16006-16011(1986).
 CC -!- FUNCTION: AMONG OTHER FUNCTIONS, SEEMS TO BE INVOLVED IN CELL
 DEATH BY APOPTOSIS. BINDS SPECIFICALLY TO G-ACTIN AND BLOCKS
 ACTIN POLYMERIZATION (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
 phosphonucleotide and 5'-phosphogluconate end-products.
 CC -!- COFACTOR: DIVALENT CATIONS PARTICULARLY CALCIUM AND MAGNESIUM.
 CC -!- SUBCELLULAR LOCATION: SECRETORY PROTEIN, STORED IN ZYMOGEN
 GRANULES AND FOUND IN THE NUCLEAR ENVELOPE.
 CC -!- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
 DR PIR; A26324; A26324.
 DR HSSP; P00639; 3DNI.
 DR InterPro; IPR001582; Dnase I.
 DR InterPro; IPR005135; Exo endo.phos.
 DR Pfam; PF03372; Exo endo.phos; 1.
 DR PRINTS; PRO0130; DNASE1.
 DR ProDom; PD005408; Dnase_I_N; 1.
 DR SMART; SM00476; DNaseIc; 1.
 DR PROSITE; PS00919; DNASE_I_1; 1.
 DR PROSITE; PS00918; DNASE_I_2; 1.
 KW Hydrolase; Endonuclease; Nuclease; Glycoprotein; Calcium;
 KW Actin-binding
 FT DISULFID 101 104
 FT DISULFID 173 209
 FT ACT SITE 78 78
 FT ACT SITE 134 134
 FT CARBOHYD 18 18
 FT CARBOHYD 106 106
 FT CARBOHYD 262 AA; 29447 MW; F83AGBDD81CD7C5 CRC64;
 SQ SEQUENCE 262 AA; 29447 MW; F83AGBDD81CD7C5 CRC64;
 Query Match 78.4%; Score 1072; DB 1; Length 262;

Best Local Similarity 77.3%; Pred. No. 2.6e-93;
 Matches 201; Conservative 30; Mismatches 29; Indels 0; Gaps 0;
 QY 1 LKIAAFNIQTGKTSNATLSYIVQILSRVDIALVOEVRDSDSLTAVGKLLDNLNQDAP 60
 DB 1 LKIAAFNIRSFQETKSNATLSYIVQILSRVDIALVOEVRDSDSLTAVGKLLDNLNEKAA 81
 QY 61 DTYHVVSPELGRKSYKERYLFVVRPDQVSAVDSYVYDDGCEPCGNDTFRPAIVRFFS 120
 DB 61 DTYHVVSPELGRKSYKERYLFVVRPDQVSAVDSYVYDDGCEPCGNDTFRPAIVRFFS 120
 QY 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVYDVOEKWGLDVMGMDFNAGCSYVRPSQ 180
 DB 121 PTKVREFAIVPLHAAPGDAVAEIDALYDVYDVOEKWGLDVMGMDFNAGCSYVRPSQ 180
 QY 181 WSSIRLWTSPTFQWMLIPDSADTTATPTCAVDRIIVVAGMLRGAVVPSALPFRFOAYG 240
 DB 181 WSSIRLWTSPTFQWMLIPDSADTTATPTCAVDRIIVVAGMLRGAVVPSALPFRFOAYG 240
 QY 241 LQDQLAQAISSDHPYVVMK 260
 DB 241 LQDQLAQAISSDHPYVVMK 260

RESULT 6

DRN1_BOVIN STANDARD; PRT; 282 AA.
 AC P00639;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Deoxyribonuclease I precursor (EC 3.1.21.1) (Dnase I).
 GN DNASE1 OR DNLI.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=98137790; PubMed=9469931;
 RA Chen C.Y., Lu S.C., Liao T.H.;
 RT "Cloning, sequencing and expression of a cDNA encoding bovine
 pancreatic deoxyribonuclease I in Escherichia coli: purification and
 characterization of the recombinant enzyme.";
 RL Gene 206:181-184(1998).
 RN [2]
 RP SEQUENCE OF 23-260.
 RX MEDLINE=73097126; PubMed=4734471;
 RA Liao T.-H., Sainikow J., Moore S., Stein W.H.;
 RT "Bovine pancreatic deoxyribonuclease A. Isolation of cyanogen bromide
 peptides, complete covalent structure of the polypeptide chain.";
 RL J. Biol. Chem. 248:1489-1495(1973).
 RN [3]
 RP REVISIONS.
 RX MEDLINE=92218466; PubMed=1348510;
 RA Liao T.-H., Sainikow J., Moore S., Stein W.H.;
 RL J. Biol. Chem. 267:7957-7957(1992).
 RN [4]
 RP VARIANT DEOXYRIBONUCLEASE C.
 RX MEDLINE=73149229; PubMed=4735137;
 RA Sainikow J., Murphy D.;
 RT "Bovine pancreatic deoxyribonuclease A and C. A proline for histidine
 substitution in deoxyribonuclease C.";
 RL J. Biol. Chem. 248:1499-1501(1973).
 RN [5]
 RP VARIANT DEOXYRIBONUCLEASE D.
 RX MEDLINE=74143471; PubMed=4856650;
 RA Liao T.-H.;
 RT "Bovine pancreatic deoxyribonuclease D.";
 RL J. Biol. Chem. 249:2354-2356(1974).
 RN [6]

Mon Nov 24 10:03:08 2003

RP ACTIVE SITE HHS-156.
RX MEDLINE=69184134; PubMed=4976790;
RA Price P.A., Moore S., Stein W.H.;
RT "Alkylation of a histidine residue at the active site of bovine
RL pancreatic deoxyribonuclease.";
RL J. Biol. Chem. 244:924-928(1969).
RN [77]
RP ACTIVE SITE TYR-87.
RX MEDLINE=72064723; PubMed=5166750;
RA Rugli T.E., Stein W.H.;
RT "Involvement of a tyrosine residue in the activity of bovine
RL pancreatic deoxyribonuclease A.";
RL J. Biol. Chem. 246:7191-7200(1971).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS).
RX MEDLINE=86230916; PubMed=3713845;
RA Suck D., Oefner C.;
RT "Structure of DNase I at 2.0-A resolution suggests a mechanism for
RL binding to and cutting DNA.";
RL Nature 321:620-625(1986).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS).
RX MEDLINE=87169744; PubMed=3560229;
RA Oefner C., Suck D.;
RT "Crystallographic refinement and structure of DNase I at 2-A
RL resolution.";
RL J. Mol. Biol. 192:605-632(1986).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS) WITH NICKED DNA OCTANUCLEOTIDE.
RX MEDLINE=88175075; PubMed=3352748;
RA Suck D., Lahm A., Oefner C.;
RT "Structure refined to 2 A of a nicked DNA octanucleotide complex with
RL DNase I.";
RL Nature 332:464-468(1988).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS).
RX MEDLINE=92085280; PubMed=1748997;
RA Lahm A., Suck D.;
RT "DNase I-induced DNA conformation. 2-A structure of a DNase I-octamer
RL complex.";
RL J. Mol. Biol. 222:645-667(1991).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=92389329; PubMed=1518054;
RA Weston S.A., Lahm A., Suck D.;
RT "X-ray structure of the DNase I-d(GGTATACC)2 complex at 2.3-A
RL resolution.";
RL J. Mol. Biol. 226:1237-1256(1992).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH ACTIN.
RX MEDLINE=90370087; PubMed=2395459;
RA Kabsch W., Mannherz H.G., Suck D., Pai E.F., Holmes K.C.;
RT "Atomic structure of the actin:DNase I complex.";
RL Nature 347:37-44(1990).
CC -1- FUNCTION: AMONG OTHER FUNCTIONS, SEEMS TO BE INVOLVED IN CELL
CC DEATH BY APOPTOSIS. BINDS SPECIFICALLY TO G-ACTIN AND BLOCKS
CC ACTIN POLYMERIZATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphonucleotide and 5'-phosphogluconucleotide end-products.
CC -1- COFACTOR: DIVALENT CATIONS, PARTICULARLY CALCIUM AND MAGNESIUM.
CC -1- SUBCELLULAR LOCATION: SECRETORY PROTEIN, STORED IN ZYMOGEN
CC GRANULES AND FOUND IN THE NUCLEAR ENVELOPE.
CC -1- PTM: THE ONLY DIFFERENCES BETWEEN THE A & B FORMS AND THE C & D
CC FORMS ARE IN THE COMPOSITIONS OF THE CARBOHYDRATE BOUND TO ASN-40.
CC -1- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
CC -1- DATABASE: NAME=Worthington enzyme manual;
CC WWW="http://www.worthington-biochem.com/manual/D/DNASE.html".
CC -----
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CC -----
CC EMBL; AJ001538; CA004819.1; -;
DR PIR; JC6532; NDBOR.
DR PDB; 1ATN; 15-JUL-92.
DR PDB; 3DNI; 31-JAN-94.
DR PDB; 2DNJ; 31-JAN-94.
DR PDB; 1DNK; 31-JAN-94.
DR InterPro; IPR001582; DNase I.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNase I_N; 1.
DR SMART; SM00476; DNaseIc; 1.
DR PROSITE; PS00918; DNASE_I_2; 1.
DR PROSITE; PS00919; DNASE_I_1; 1.
KW Hydroxylase; Endonuclease; Nuclease; Glycoprotein; Calcium;
KW Apoptosis; Actin-binding; Signal; Polymorphism; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 282 DEOXYRIBONUCLEASE I.
FT ACT_SITE 100 100
FT ACT_SITE 156 156
FT SITE 35 35 INVOLVED IN ACTIN-BINDING.
FT SITE 89 89 INVOLVED IN ACTIN-BINDING.
FT CARBOHYD 40 40 N-LINKED (GLUCNA...)
FT VARIANT 143 143 H -> P (IN C AND D FORMS).
FT STRAND 24 33
FT HELIX 35 38
FT TURN 39 39
FT HELIX 41 51
FT TURN 52 53
FT STRAND 56 62
FT TURN 65 66
FT HELIX 68 77
FT TURN 78 78
FT TURN 82 83
FT STRAND 86 89
FT STRAND 93 93
FT STRAND 100 106
FT TURN 108 110
FT STRAND 111 118
FT STRAND 136 142
FT STRAND 149 154
FT HELIX 159 161
FT STRAND 162 180
FT STRAND 185 190
FT TURN 195 197
FT HELIX 200 205
FT HELIX 207 210
FT TURN 212 213
FT STRAND 215 216
FT TURN 220 221
FT STRAND 225 225
FT STRAND 234 239
FT HELIX 241 246
FT STRAND 247 247
FT TURN 249 250
FT STRAND 253 254
FT HELIX 257 261
FT TURN 262 262
FT HELIX 265 271
FT STRAND 274 274
FT STRAND 277 282
SQ SEQUENCE 282 AA; 31345 MW; 43904EP0D5F2E0E2 CRC64;
Query Match 78.1%; Score 1067; DB 1; Length 282;
Best Local Similarity 78.0%; Pred. No. 8.3e-93;
Matches 203; Conservative 28; Mismatches 29; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLSYIVQILSRDYALQVEVDSHULTAVGKLLDNLNQADP 60
 DB 23 LKIAAFNIQTGETKMSNATLSYIVRIRYDVLQVEVDSHULTAVGKLLDNLNQADP 82
 QY 61 DTYHVVSEPLGRKSYKERYLFVYRPPDOVSADVSYVDGCEPCGNDTFNREPAIVRFFS 120
 DB 83 NTHYHVVSEPLGRNSYKERYLFVYRPPDOVSADVSYVDGCEPCGNDTFNREPAIVRFFS 142
 QY 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVLVDQVEKMGLEDVLMGDFNAGCSYVRPSQ 180
 DB 143 HSTVKKEFAIVLHSAAPSADVAEINSLYDVLVDQVKHLDVLMGDFNAGCSYVRPSQ 202
 QY 181 WSSIRLWTSPTFQWMLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPENFOAYG 240
 DB 203 WSSIRLWTSPTFQWMLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPENFOAYG 262
 QY 241 LSDQLAQAISSHYPVEVNL 259
 DB 263 LSNEMALAISSHYPVEVNL 281

RESULT 7
 DRNL SHEEP STANDARD; PRT; 260 AA.
 AC P11937.
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Deoxyribonuclease I (EC 3.1.21.1) (DNase I).
 GN DNASE1 OR DNLI.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=87057261; PubMed=3782105;
 RA Paul H.K., Liao T.-H.;
 RT "Comparison of the three primary structures of deoxyribonuclease
 RT isolated from bovine, ovine, and porcine pancreas. Derivation of the
 RT amino acid sequence of ovine DNase and revision of the previously
 RT published amino acid sequence of bovine DNase."
 RL J. Biol. Chem. 261:16012-16017(1986).
 CC -!- FUNCTION: AMONG OTHER FUNCTIONS, SEEMS TO BE INVOLVED IN CELL
 CC DEATH BY APOPTOSIS. BINDS SPECIFICALLY TO G-ACTIN AND BLOCKS
 CC ACTIN POLYMERIZATION (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
 CC phosphodinucleotide and 5'-phosphooligonucleotide end-products.
 CC -!- COFACTOR: DIVALENT CATIONS, PARTICULARLY CALCIUM AND MAGNESIUM.
 CC -!- SUBCELLULAR LOCATION: SECRETORY PROTEIN, STORED IN ZYMOGEN
 CC GRANULES AND FOUND IN THE NUCLEAR ENVELOPE.
 CC -!- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
 CC PIR, B26325; B26325.
 DR HSP; P00639; 3DN1.
 DR InterPro; IPR001582; DNase I.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR PRINTS; PR00130; DNASE1.
 DR ProDom; PD005408; DNase_I_N; 1.
 DR SMART; SM00476; DNaseIc; 1.
 DR PROSITE; PS00919; DNASE_I_1; 1.
 DR PROSITE; PS00918; DNASE_I_2; 1.
 KW Hydrolase; Endonuclease; Nuclease; Glycoprotein; Calcium;
 KW Apoptosis; Actin-binding.
 FT DISULFID 101 104
 FT BY SIMILARITY.
 FT ESSENTIAL FOR ENZYMACTIC ACTIVITY
 FT (BY SIMILARITY).
 FT ACT SITE 78 78
 FT ACT SITE 134 134
 FT BY SIMILARITY.
 FT CARBOHYD 18 18
 FT N-LINKED (GLCNAC. . .).

FT VARIANT 163 163 I -> V (IN MINOR VARIANT).
 SQ SEQUENCE 260 AA; 28939 MW; B1B4D2C50DA3BF20 CRC64;
 Query Match 77.6%; Score 1061; DB 1; Length 260;
 Best Local Similarity 77.2%; Pred. No. 2.7e-92;
 Matches 200; Conservative 32; Mismatches 27; Indels 0; Gaps 0;
 QY 1 LKIAAFNIQTGETKMSNATLSYIVQILSRDYALQVEVDSHULTAVGKLLDNLNQADP 60
 DB 1 LKIAAFNIQTGETKMSNATLSYIVRIRYDVLQVEVDSHULTAVGKLLDNLNQADP 60
 QY 61 DTYHVVSEPLGRKSYKERYLFVYRPPDOVSADVSYVDGCEPCGNDTFNREPAIVRFFS 120
 DB 61 NTHYHVVSEPLGRNSYKERYLFVYRPPDOVSADVSYVDGCEPCGNDTFNREPAIVRFFS 120
 QY 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVLVDQVEKMGLEDVLMGDFNAGCSYVRPSQ 180
 DB 121 HSTVKKEFAIVLHSAAPSADVAEINSLYDVLVDQVKHLDVLMGDFNAGCSYVRPSQ 180
 QY 181 WSSIRLWTSPTFQWMLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPENFOAYG 240
 DB 181 WSSIRLWTSPTFQWMLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPENFOAYG 240
 QY 241 LSDQLAQAISSHYPVEVNL 259
 DB 241 LSNEMALAISSHYPVEVNL 259

RESULT 8
 DRNL CHICK STANDARD; PRT; 282 AA.
 AC Q9YGF5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Deoxyribonuclease I precursor (EC 3.1.21.1) (DNase I).
 GN DNASE1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Lu S.C., Hu C.C., Liao T.H.;
 RT "Chicken pancreatic deoxyribonuclease I: purification and
 RT characterization as well as cloning, sequence and expression of its
 RT gene."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AMONG OTHER FUNCTIONS, SEEMS TO BE INVOLVED IN CELL
 CC DEATH BY APOPTOSIS. BINDS SPECIFICALLY TO G-ACTIN AND BLOCKS ACTIN
 CC POLYMERIZATION (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
 CC phosphodinucleotide and 5'-phosphooligonucleotide end-products.
 CC -!- COFACTOR: DIVALENT CATIONS, PARTICULARLY CALCIUM AND MAGNESIUM (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SECRETORY PROTEIN, STORED IN ZYMOGEN
 CC GRANULES AND FOUND IN THE NUCLEAR ENVELOPE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ131751; CAA10503.1; ..
 DR HSP; P00639; LDNK.
 DR InterPro; IPR001582; DNase I.
 DR InterPro; IPR005135; Exo_endo_phos.

DR Pfam: PF003372; Exo endo_phos; 1.
 DR PRINTS; PR00130; DNaseI.
 DR ProDom; PD005408; DNase_I_N; 1.
 DR SMART; SM00476; DNaseIc; 1.
 DR PROSITE; PS00919; DNase_I_1; FALSE NEG.
 DR PROSITE; PS00918; DNase_I_2; 1.
 KW Hydrolase; Endonuclease; Nuclease; Glycoprotein; Calcium; Signal;
 KW Apoptosis; Actin-binding.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 282 DEOXYRIBONUCLEASE I.
 FT DISULFID 121 124 BY SIMILARITY.
 FT DISULFID 193 229 ESSENTIAL FOR ENZYMIC ACTIVITY
 (BY SIMILARITY).
 FT ACT SITE 98 98 BY SIMILARITY.
 FT ACT SITE 154 154 BY SIMILARITY.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 282 AA; 31400 MW; 2226267860842EA7 CRC64;
 Query Match 55.7%; Score 762; DB 1; Length 282;
 Best Local Similarity 58.1%; Pred. No. 3.6e-64;
 Matches 151; Conservative 34; Mismatches 75; Indels 0; Gaps 0;
 QY 1 LKTAENIOTFGTGMNATLYSVIQLSRVDIALVOEVRDLSHTAVGKLLDNLNODAP 60
 DB 21 LKTAENIOTFGTGMNATLYSVIQLSRVDIALVOEVRDLSHTAVGKLLDNLNODAP 60
 QY 61 DTYHYVSEPLGRKSKYKERYLFVYRDPQSAVDSDYDDGCEPCGNDTFNREPAIVRFS 120
 DB 81 YPYSFLSSIPGRKSKYKERYLFVYRDPQSAVDSDYDDGCEPCGNDTFNREPAIVRFS 140
 QY 121 RFTVEFEAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEVDVLMGDFNAGCSYVRSQ 180
 DB 141 PTQDEFVIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEVDVLMGDFNAGCSYVRSQ 200
 QY 181 WSIRLWTSFTQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPDSALPFPQAAAYG 240
 DB 201 WPSIRLSLSCENLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPDSALPFPQAAAYG 260
 QY 241 LSDQLAQASDHPVVEVMLK 260
 DB 261 IQNKDALAISDHPVVEVTLK 280

RESULT 9

DRNL OREMO
 ID DRNL OREMO STANDARD; PRT; 284 AA.
 AC Q42456;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neoxryibonuclease I precursor (EC 3.1.21.1) (Dnase I).
 OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
 CC Cichlidae; Oreochromis.
 OC NCBI_TaxID=8127;
 RN [1]
 SEQUENCE FROM N.A.; SEQUENCE OF 27-284, AND CHARACTERIZATION.
 RP TISSUE=Hepatopancreas;
 RX MEDLINE=98055705; PubMed=9395327;
 RA Hsiao Y.-M., Ho H.-C., Wang W.-Y., Tam M.F., Liao T.-H.;
 RT "Purification and characterization of tilapia (Oreochromis mossambicus) deoxyribonuclease I. Primary structure and cDNA sequence.";
 RT Eur. J. Biochem. 249:786-791(1997).
 RL CC -1- FUNCTION: AMONG OTHER FUNCTIONS, SEEMS TO BE INVOLVED IN CELL DEATH BY APOPTOSIS. BINDS SPECIFICALLY TO G-ACTIN AND BLOCKS ACTIN POLYMERIZATION. PREFERENTIALLY ATTACKS DOUBLE-STRANDED DNA AND PRODUCES OLIGONUCLEOTIDES WITH 5'-PHOSPHO AND 3'-HYDROXY TERMINI.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-phosphonucleotide and 5'-phosphooligonucleotide end-products.
 CC -1- COFACTOR: DIVALENT CATIONS, PARTICULARLY CALCIUM AND MAGNESIUM

CC WHICH HAVE A SYNERGISTIC EFFECT ON ACTIVATION.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: SECRETORY PROTEIN, STORED IN ZYMOGEN GRANULES AND FOUND IN THE NUCLEAR ENVELOPE (BY SIMILARITY).
 CC -1- MISCELLANEOUS: MOST ACTIVE AT PH 8.5.
 CC -1- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
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 CC EMBL; AJ001305; CAA04665.1; .
 DR HSSP; P00639; 3DNI.
 DR InterPro; IPR001582; DNase I.
 DR Pfam; PF003372; Exo_endo_phos; 1.
 DR PRINTS; PR00130; DNaseI.
 DR ProDom; PD005408; DNase_I_N; 1.
 DR SMART; SM00476; DNaseIc; 1.
 DR PROSITE; PS00919; DNase_I_1; 1.
 DR PROSITE; PS00918; DNase_I_2; 1.
 KW Hydrolase; Endonuclease; Nuclease; Glycoprotein; Calcium; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 284 DEOXYRIBONUCLEASE I.
 FT ACT SITE 103 103 BY SIMILARITY.
 FT ACT SITE 159 159 BY SIMILARITY.
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. .).
 FT VARIANT 151 151 R -> K.
 SQ SEQUENCE 284 AA; 32215 MW; D5154AP0C782B595 CRC64;
 Query Match 53.8%; Score 736; DB 1; Length 284;
 Best Local Similarity 54.8%; Pred. No. 1e-61;
 Matches 142; Conservative 44; Mismatches 71; Indels 2; Gaps 2;
 QY 1 LKTAENIOTFGTGMNATLYSVIQLSRVDIALVOEVRDLSHTAVGKLLDNLNODAP 60
 DB 27 LLGAENIKSFGDTKASNAITLNIITKIVKRVIVDILIOEVRDLSHTAVGKLLDNLNODAP 86
 QY 61 DTYHYVSEPLGRKSKYKERYLFVYRDPQSAVDSDYDDGCEPCGNDTFNREPAIVRFS 120
 DB 87 Q-YKIVSEPLGASTYKERYLFYREALVSVKSYTYDDGPEETGDTFSRPFVYVWFSS 145
 QY 121 RFTVEFEAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEVDVLMGDFNAGCSYVRSQ 180
 DB 146 KNTAVADFTLIPQHTSPDLAVRELNALYDVLDVLRARNTNDIVLIGDFNAGCSYVSGSA 205
 QY 181 WSIRLWTSFTQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPDSALPFPQAAAYG 240
 DB 206 WQIRIFDTKTHLITDAADTTVSTQVCPYDRIVVTDMRG-VVQNSAKVYNYMTDLN 264
 QY 241 LSDQLAQASDHPVVEVML 259
 DB 265 LKODLALAVSDHPVVEVKL 283
 RESULT 10
 DRNL HUMAN
 ID DHPI HUMAN STANDARD; PRT; 299 AA.
 AC Q2874;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Dnase I homolog protein, DHPI precursor (EC 3.1.21.-).
 GN DNASE1L2 OR DNASE1L2 OR DHPI.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]

RESULT 11

-!- FUNCTION: HAS DNA HYDROLYTIC ACTIVITY. DOES NOT BIND TO ACTIN.
-!- SUBCELLULAR LOCATION: NUCLEAR; MAY FIRST PASS THROUGH THE ER
MEMBRANE BEFORE BEING IMPORTED IN THE NUCLEUS (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER AND SPLEEN.
-!- SIMILARITY: BELONGS TO THE DNASE I FAMILY.

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EMBL; AF047355; AAC35753.1; -.
HSSP; P00639; 3DNI.
MGD; MGI:1314633; Dnase1l3.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0004519; F:endonuclease activity; IDA.
GO; GO:0006315; P:apoptosis; IDA.
GO; GO:0006309; P:DNA fragmentation; IDA.
InterPro; IPR001582; DNase_I.
InterPro; IPR005135; Exo_endo_phos.
PFAM; PF03372; Exo_endo_phos; 1.
PRINTS; PR00130; DNASEI_
ProDom; PD005408; DNase_I_N; 1.
SMART; SM00476; DNaseIc; 1.
PROSITE; PS00918; DNASE_I_2; 1.
PROSITE; PS00919; DNASE_I_1; 1.
Hydrolase; Endonuclease; Nuclease; Signal; Nuclear protein;
Apoptosis.
1 25 BY SIMILARITY.
SIGNAL

```

Query Match      51.5%; Score 704.5; DB 1; Length 299;
Best Local Similarity 51.1%; Prd. NO. 9.8e-59;
Matches 143; Conservative 38; Mismatches 74; Indels 25; Gaps 2;

QY 1 LKIAAFNIQTGFTKMSNATLVSYVQILRSYDIALVQVEVRSDLTAVGKLLDNENQADP 60
DB 22 LRIAGFIQTGFGSKVSDPACGIIAKIILAGYDLALVQVEVDPOLSAVSALMEQINSVE 81

```

FT CHAIN 26 310 DEOXYRIBONUCLEASE GAMMA.
 FT DOMAIN 40 56
 FT PARTIAL SEQUENCE, AND CHARACTERIZATION.
 FT MEDLINE=97469339; Pubmed=9328279;
 FT "Purification, characterization, and amino acid sequencing of DNase gamma from rat spleen."
 FT RA Shiohawa D., Iwamatsu A., Tanuma S.-I.;
 FT "Purification, characterization, and amino acid sequencing of DNase gamma from rat spleen."
 FT RT thymocytes."
 FT Biochem. J. 332:713-720 (1998).
 SQ SEQUENCE 310 AA; 35760 MW; BE463821E045E374 CRC64;
 Query Match 44.0%; Score 601; DB 1; Length 310;
 Best Local Similarity 46.4%; Pred. No. 5.4e-49;
 Matches 122; Conservative 45; Mismatches 92; Indels 4; Gaps 3;
 QY 1 LKTAAPNIQTFGTGKSNATLSYIVQILSRVDIALVQVRSVSHLTAVGKLLDNQDA- 59
 DB 26 LRLCSFNVRSGFSGSKENHEAMDIIVKIKRCDLILLMEIKDSSNNICPMLMEKLNISR 85
 QY 60 -PTTHYHVVSEPLGRSYTERILFVIRPQVGAVDSSYYDDCCGCGNDTFREPAIVRF 118
 DB 86 RSTYNYVISRLGRNTYKEQAFVYKELVSKTKYHYHD-YQDGDVDFSRPFVYWF 144
 QY 119 FSRFTEVREFAIVPLHAAPGDAVAEIDALYDVLDVQVEKGLDVMGMDFNAGCSYVRP 178
 DB 145 HSFTAVKDVIVPLHTTETSKEIDELVDVTVDRSQWKTENIFMGDFNAGCSYVPK 204
 QY 179 SOWSSIRLWTSPTFQWLPIDSDTTA-TPTHGAYRIVVAGMLRGAVVDPDSALPFFQA 237
 DB 205 KAWGNIRLDRPXFVWLGQDQEDTVTKKTSCTSCAYDRVLCGQEVINVSVRSSGVDFRQK 264
 QY 238 AYGLSDQLAQAIQSHVPEVMK 260
 DB 265 AYDLSEEDLDVSDHFFVEPKLQ 287

RESULT 12

DRNG RAT STANDARD; PRT; 310 AA.
 AC 089107;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Deoxyribonuclease gamma precursor (EC 3.1.21.-) (DNase gamma)
 DE (Deoxyribonuclease I-like 3) (DNaseY).
 GN DNASE1L3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 {1}
 RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RP STRAIN=Sprague-Dawley; TISSUE=Liver;
 RC MEDLINE=98332537; Pubmed=9665719;
 RX Liu Q.Y., Pandey S., Singh R.K., Lin W., Ribocco M.,
 RA Borow-Borowski H., Smith B., Leblanc J., Walker P.R., Sikorska M.;
 RT "DNaseY: a rat DNaseI-like gene coding for a constitutively expressed
 RT chromatin-bound endonuclease."
 RL Biochemistry 37:10134-10143 (1998).
 {2}
 RN SEQUENCE FROM N.A.
 RP STRAIN=Sprague-Dawley; TISSUE=Spleen;
 RC MEDLINE=98285539; Pubmed=9620874;
 RX Shiohawa D., Tanuma S.-I.;
 RA "Molecular cloning and expression of a cDNA encoding an apoptotic
 RT endonuclease DNase gamma."
 RT Biochem. J. 332:713-720 (1998).
 {3}
 RN PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RP TISSUE=Spleen;
 RC MEDLINE=97469339; Pubmed=9328279;
 RX Shiohawa D., Iwamatsu A., Tanuma S.-I.;
 RA "Purification, characterization, and amino acid sequencing of DNase
 RT gamma from rat spleen."
 RT Biochem. J. 332:713-720 (1998).

RL Arch. Biochem. Biophys. 346:15-20 (1997).
 {4}
 RN PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RP MEDLINE=97439708; Pubmed=9307016;
 RX Shiohawa D., Onyama H., Yamada T., Tanuma S.-I.;
 RA "Purification and properties of DNase gamma from apoptotic rat
 RT thymocytes."
 RT Biochem. J. 326:675-681 (1997).
 {5}
 RN FUNCTION
 RP STRAIN=Sprague-Dawley; TISSUE=Spleen;
 RC MEDLINE=95045534; Pubmed=7937253;
 RA Shiohawa D., Onyama H., Yamada T., Takahashi K., Tanuma S.-I.;
 RT "Identification of an endonuclease responsible for apoptosis in rat
 RT thymocytes."
 RT Eur. J. Biochem. 226:23-30 (1994).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE EARLY STAGES OF APOPTOTIC DNA
 CC FRAGMENTATION. IS CAPABLE OF BOTH SINGLE- AND DOUBLE-STRANDED DNA
 CC CLEAVAGE, PRODUCING DNA FRAGMENTS WITH 3'-OH ENDS.
 CC -1- COFACTOR: CALCIUM/MAGNESIUM IONS-DEPENDENT.
 CC -1- ENZYME REGULATION: INHIBITED BY ZINC.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; MAY FIRST PASS THROUGH THE ER
 CC MEMBRANE BEFORE BEING IMPORTED IN THE NUCLEUS.
 CC -1- TISSUE SPECIFICITY: DETECTED AT HIGH LEVELS IN SPLEEN, LYMPH
 CC NODES, THYMUS AND LIVER. OBSERVED ALSO IN KIDNEY AND TESTIS BUT
 CC NOT IN BRAIN OR HEART.
 CC -1- PFM: SEEMS TO BE SYNTHESIZED AS AN INACTIVE PRECURSOR PROTEIN AND
 CC CONVERTED INTO AN ACTIVE MATURE ENZYME BY REMOVAL OF THE N-
 CC TERMINAL PRECURSOR PEPTIDE DURING APOPTOSIS.
 CC -1- MISCELLANEOUS: ACTIVE OVER A BROAD PH RANGE (OPTIMUM PH 7-8).
 CC -1- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF039852; AAC28937.1; -
 CC EMBL; U75689; AAC40134.1; -
 CC HSSP; P00639; 3DNI.
 CC InterPro: IPR001582; DNase I.
 CC InterPro: IPR005135; Exo endo phos.
 CC Pfam: PF03372; Exo endo phos; 1.
 CC PRINTS: PR00130; DNASEL_I_N; 1.
 CC PRODOM: PD005408; DNase_I_N; 1.
 CC SMART; SM00476; DNaseic; 1.
 CC PROSITE; PS00919; DNASE_I_1; 1.
 CC PROSITE; PS00918; DNASE_I_2; 1.
 CC Hydrolase; Endonuclease; Nuclease; Signal; Nuclear protein;
 CC Apoptosis.
 CC SIGNAL 1 25 DEOXYRIBONUCLEASE GAMMA.
 CC CHAIN 26 310 BIPARTITE NUCLEAR LOCALIZATION SIGNAL
 CC DOMAIN 40 56 (POTENTIAL).
 CC DOMAIN 301 307 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC DISULFID 199 236 ESSENTIAL FOR ENZYMACTIC ACTIVITY
 CC ACT SITE 105 105 (BY SIMILARITY).
 CC ACT_SITE 160 160 BY SIMILARITY.
 CC SEQUENCE 310 AA; 35708 MW; 69C0E0874A3E9107 CRC64;
 Query Match 43.4%; Score 593; DB 1; Length 310;
 Best Local Similarity 45.6%; Pred. No. 3e-48;
 Matches 120; Conservative 47; Mismatches 92; Indels 4; Gaps 3;
 QY 1 LKTAAPNIQTFGTGKSNATLSYIVQILSRVDIALVQVRSVSHLTAVGKLLDNQDA- 59
 DB 26 LRLCSFNVRSGFSGSKENHEAMDIIVKIKRCDLILLMEIKDSSNNICPMLMEKLNISR 85

Db 200 KAMKNIIRLRTPDFVWLGIDQSDTTVKKSTNCAYDRIVLRGQEIYVSSVVPKSNVSFDFQX 259
 Qy 238 AYGLSDQLAQATSDHVPVEVMLK 260
 Db 260 AYKLTBEALDVSDHPPVEFKLQ 282

RESULT 14

DNML_HUMAN STANDARD; PRT; 302 AA.
 AC P49184;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Muscle-specific DNase I-like precursor (EC 3.1.21.-) (DNase X) (X1B).
 GN DNASE1L1 OR DNASE1L4 OR DNML.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA Coy J.F.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN 12;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=96081217; PubMed=8541839;
 RA Parrish J.E., Ciccodicola A., Wehnert M., Cox G.F., Chen E.,
 RA Nelson D.L.;
 RT "A muscle-specific DNase I-like gene in human Xq28";
 RL Hum. Mol. Genet. 4:1557-1564 (1995).
 RN 13;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96311563; PubMed=8733135;
 RA Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.-N.,
 RA Zuo L., Heiner C., Burrough F.W., Ripetto M., Schlessinger D.,
 RA D'Urso M.;
 RT "Long-range sequence analysis in Xq28: thirteen known and six
 candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and
 G6PD loci";
 RL Hum. Mol. Genet. 5:659-668 (1996).
 RN 14;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=96194910; PubMed=8654957;
 RA Pergolizzi R., Appierto V., Bosetti A., Debellis G.L., Rovida E.,
 RA Blunio I.;
 RT "Cloning of a gene encoding a DNase I-like endonuclease in the human
 Xq28 region";
 RL Gene 168:267-270 (1996).
 RN 15;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood, and Cervix;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matovina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Teichgraber S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
 CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN SKELETAL AND CARDIAC MUSCLE.
 CC DETECTABLE IN ALL OTHER TISSUES TESTED EXCEPT BRAIN.
 CC -!- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
 CC -----
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 CC -----

EMBL; X90392; CAA62037.1; -
 EMBL; L40817; AAB00495.1; -
 EMBL; L40823; AAB00496.1; -
 EMBL; L44140; AAB02647.1; -
 EMBL; U06846; AAB17022.1; -
 EMBL; BC001561; AAB01561.1; -
 EMBL; BC028092; AAB28092.1; -
 EMBL; J04633; J04633.
 DR HSP; P00639; 2DNJ.
 DR HSP; P00639; 2DNJ.
 DR GENE; HGNC:2957; DNASE1L1.
 DR MIM; 300081; -
 DR GO; GO:0004536; F:deoxyribonuclease activity; TAS.
 DR InterPro; IPR001582; DNase I.
 DR InterPro; IPR001535; Exo endo phos.
 DR Pfam; PF03372; Exo endo phos; 1.
 DR PRINTS; PR00130; DNASEI.
 DR ProDom; PD005408; DNaseI_N; 1.
 DR SMART; SM00476; DNaseIc; 1.
 DR PROSITE; PS00918; DNASEI_2; 1.
 DR PROSITE; PS00919; DNASEI_1; 1.
 DR KEGG; Hydroxylase; Endonuclease; Nuclease; Glycoprotein; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 302 MUSCLE-SPECIFIC DNASE I-LIKE
 FT DISULFID 187 224 ESSENTIAL FOR ENZYMACTIC ACTIVITY
 FT ACT_SITE 97 97 BY SIMILARITY.
 FT ACT_SITE 148 148 BY SIMILARITY.
 FT CARBOHYD 261 261 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 73 73 L -> I (IN REF. 2; AAB00496).
 FT CONFLICT 78 78 G -> D (IN REF. 2; AAB00496).
 FT CONFLICT 205 205 G -> S (IN REF. 2; AAB00496).
 FT CONFLICT 227 227 D -> A (IN REF. 2; AAB00495 AND 3).
 SQ SEQUENCE 302 AA; 33892 MW; D10CEB8470173727 CRC64;

Query Match 34.0%; Score 464.5; DB 1; Length 302;
 Best Local Similarity 38.7%; Pred. No. 3.4e-36;
 Matches 101; Conservative 48; Mismatches 103; Indels 9; Gaps 4;
 Qy 2 KIAENIOTFGTEKSNATLVSYIYQILSRDYALVQSVROSHLTAVGKLLDNLNQ-DAP 60
 Db 20 RICAFNAQRLTAKVAREQVMDTLKRLARCIMVLQEVVDSSGSAIFLLRLNRFDS 79
 Qy 61 DTHYVVSPLGRKSKYKERYLFVYRPOQVSAVDVSYDDGCEPCGNDTFNREPAIVRFS 120
 Db 80 GPYSTLSQQLGRSTMEYVYFYSKTKVQLSSVYND-----EDDVFAEPPFAQFSL 134
 Qy 121 RFEVREPAIVLHAAPGDVAEIDALVDYLDVQKVGLEDVLMGDFNAGCSYVRPSQ 180
 Db 135 PSNVLPVSLVPLHTTPKAVEKELNLYDVFLEVSQHWKSDVILLGDFNADCASLTAKR 194
 Qy 181 WSSIRLWTSPTQWLIPDSADTTA-TPTHCAVORTVWAGMLRGVAVPDSALPFRQAY 239
 Db 195 LDKLERTTEFGHWIADSDTTVASTHTCTVDRVVLNGRCRSL--HTAAAFDPTSF 252
 Qy 240 GLSDQLAQATSDHVPVEVMLK 260
 Db 253 QLTEBEALNISDHPVEVMLK 273

RESULT 15
RRPO_CGMVS STANDARD; PRT: 1648 AA.
ID RRPO_CGMVS STANDARD; PRT: 1648 AA.
AC P19523; P89877; P90356; Q83208;
DT 01-FEB-1991 (Rel. 17, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (186 kDa protein) [Contains:
Methyltransferase/RNA helicase (MT/HEL) (129 kDa protein)].
OS Cucurbit green mottle mosaic virus (watermelon strain SH) (CGMWV), and
OS Cucurbit green mottle mosaic virus (watermelon strain W) (CGMWV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12236, 12237;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SH;
RX MEDLINE=91311400; PubMed=1856687;
RA Ugaki M., Tomiyama M., Kakutani T., Hidaka S., Kiguchi T., Nagata R.,
RA Sato T., Motoyoshi F., Nishiguchi M.;
RT "The complete nucleotide sequence of cucumber green mottle mosaic
virus (SH strain) Genomic RNA.";
RL J. Gen. Virol. 72:1487-1495 (1991).
RN [2]
RP REVISIONS.
RC STRAIN=SH;
RA Ugaki M., Tomiyama M., Kakutani T., Hidaka S., Kiguchi T., Nagata R.,
RA Sato T., Motoyoshi F., Nishiguchi M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 1496-1648 FROM N.A.
RC STRAIN=W;
RX MEDLINE=89073773; PubMed=3201760;
RA Saito T., Imai Y., Meshi T., Okada Y.;
RT "Interviral homologues of the 30K proteins of tobamoviruses";
RL Virology 167:653-656 (1988).
CC -!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
RNA REPLICATION.
CC -!- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
CAPING AND AN RNA HELICASE.
CC -!- CATALYTIC ACTIVITY, N nucleoside triphosphate = N diphosphate +
{RNA} (N).
CC -!- MISCELLANEOUS: REACTTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
CODONS FOR LYS-1144 AND GLN-1146.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; D12505; BAA18895.1; -;
CC EMBL; D12505; BAA18895.1; -;
CC EMBL; J04322; BAA46382.1; -;
CC PIR; J01157; WMTMS2.
CC InterPro; IPR001788; RNA_dep_RNAPol2.
CC InterPro; IPR007095; RNA_pol_DS_PS.
CC InterPro; IPR007094; RNA_pol_PSVir.
CC InterPro; IPR002588; V_methyltransf.
CC InterPro; IPR000606; Viral_helicase1.
CC Pfam; PF00978; RNA_dep_RNAPol2; 1.
CC Pfam; PF01443; Viral_helicase1; 1.
CC Pfam; PF01660; Vmethyltransf; 1.
KW Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
FT CHAIN 1 1648 RNA-DIRECTED RNA POLYMERASE.
FT CHAIN 1 1144 METHYLTRANSFERASE/RNA HELICASE.
FT NP_BIND 863 870 ATP (POTENTIAL).
SQ SEQUENCE 1648 AA; 186549 MW; 1D1AFEEETB65595 CRC64;

Query Match

7.4%; Score 100.5; DB 1; Length 1648;

Best Local Similarity 22.9%; Pred. No. 0.44;
Matches 56; Conservative 37; Mismatches 81; Indels 71; Gaps 14;
QY 46 TAVGKLLDNLNODAP--DTY-HYVVSEPLGR-----KSKERYLFFVVRPOVSA-----91
DB 1313 SAVGQLANFNFDLPADFYMIMIKQPKSRDLDTISQSEYPALQITIVHPKVVNAVFGPV 1372
QY 92 -----VDS-----YYVDGCEPCGNDTFNREPAIVRPFSEFRTEVREFAIVELHAAP 137
DB 1373 FKYLTTKFLSMVDSSKFFV-----TRKPEDLQERPSDLSSSHSDVEILELVSK 1422
QY 138 GDAVAIDALDYVLQVQKNGLEDVM-----LMGDFNAGCS-----YVRFPSQWS 182
DB 1423 YDK-SQSDFFHSIEMAIWEKLGDLDDILAMWMSGHKRTILQDFQAGIKTLIYYQKS--G 1479
QY 183 SIRLWTSPTF-----QMLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPD-----SALP 232
DB 1480 DVTFPIGNTFIINACVASMLP--LDKCPKASEGDDSLI---YLPKGLXPDIQATNIV 1534
QY 233 FNFOA 237
DB 1535 WNFEA 1539

Search completed: November 21, 2003, 13:55:40
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 13:45:30 ; Search time 40 Seconds
(without alignments)
1677.342 Million cell updates/sec

Title: US-10-005-306-9
Perfect score: 1367
Sequence: 1 LKTAARNIQTFFGTSMNAT.....LSDLQAIAISDHYPVEVMLK 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1131	82.7	284	11 Q91WL7	Q91WL7 mus musculus
2	1099	80.4	284	6 Q95KK2	Q95KK2 sus scrofa
3	1097	80.2	332	11 Q8K0U1	Q8K0U1 mus musculus
4	1064	77.8	282	6 Q8M027	Q8M027 bos taurus
5	1060	77.5	272	6 Q9GL63	Q9GL63 bos taurus
6	804	58.8	282	13 Q90YA9	Q90YA9 elaphe clim
7	801	58.6	282	13 Q8UWB6	Q8UWB6 agkistrodon
8	759	55.5	283	13 Q9PTY8	Q9PTY8 gallus gall
9	748	54.7	279	13 Q8JIP7	Q8JIP7 cyprinus ca
10	694.5	50.8	278	11 Q9D1G0	Q9D1G0 mus musculus
11	678.5	49.6	278	11 Q9B645	Q9B645 mus musculus
12	671.5	49.1	353	13 Q9QWM1	Q9QWM1 rana catesb
13	666.5	48.8	353	13 Q9QWM0	Q9QWM0 bufo japoni
14	628.5	46.0	350	13 Q9BEG8	Q9BEG8 xenopus lae
15	628	45.9	295	13 Q9Y1O4	Q9Y1O4 xenopus lae
16	626.5	45.8	350	13 Q9PTX0	Q9PTX0 xenopus lae

17	613.5	44.9	354	13 Q90W31	Q90W31 cyndops pyrr
18	595	43.5	310	11 Q91X38	Q91X38 mus musculu
19	477	34.9	314	11 Q9D7J6	Q9D7J6 mus musculu
20	161	11.8	47	6 Q9TQX9	Q9TQX9 bos taurus
21	158.5	11.6	279	16 Q8R5P1	Q8R5P1 fusobacteri
22	128	9.4	1067	16 Q9ZQ33	Q9ZQ33 deinococcus
23	100.5	7.4	1648	12 Q8QTJ1	Q8QTJ1 cucumber gr
24	100.5	7.4	1648	12 Q8QTJ9	Q8QTJ9 cucumber gr
25	100.5	7.4	1648	12 Q9IR66	Q9IR66 cucumber gr
26	94.5	6.9	289	2 Q32586	Q32586 escherichia
27	94	6.9	1070	2 Q44070	Q44070 aeromonas h
28	93	6.8	850	16 Q8FML9	Q8FML9 corynebacte
29	91.5	6.7	916	16 Q8NM11	Q8NM11 corynebacte
30	91.5	6.7	1317	10 Q8SA85	Q8SA85 zea mays (m
31	91	6.7	488	3 Q74867	Q74867 schizosacch
32	91	6.7	761	16 Q8Y2X4	Q8Y2X4 anabaena sp
33	91	6.7	1257	4 Q43738	Q43738 homo sapien
34	91	6.7	1917	4 Q9H1I9	Q9H1I9 homo sapien
35	91	6.7	2202	4 Q8K3C0	Q8K3C0 homo sapien
36	90	6.6	337	16 Q9KM91	Q9KM91 vibrio chol
37	89.5	6.5	459	16 Q8D9K3	Q8D9K3 vibrio vuln
38	89	6.5	2157	10 Q9FNQ1	Q9FNQ1 arabidopsis
39	88.5	6.5	534	16 Q8ZC03	Q8ZC03 versinia pe
40	88.5	6.5	534	16 Q8CLM3	Q8CLM3 versinia pe
41	88	6.4	929	2 Q32491	Q32491 bacteroides
42	87	6.4	441	10 Q9ZV44	Q9ZV44 arabidopsis
43	87	6.4	441	10 Q8H153	Q8H153 arabidopsis
44	87	6.4	745	10 Q942W5	Q942W5 oryza sativ
45	87	6.4	779	16 Q9HX44	Q9HX44 pseudomonas

ALIGNMENTS

RESULT 1

Q91WL7 ID Q91WL7 PRELIMINARY; PRT; 284 AA.
AC Q91WL7; 2001 (T-REMBLrel. 19, Created)
DT 01-DEC-2001 (T-REMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-REMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-REMBLrel. 23, Last annotation update)
DE Similar to deoxyribonuclease I.
GN DNASEI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (0CT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC014718; AAH14718.1; -;
DR MGD; MGI:103157; DnaseI.
DR InterPro; IPR001582; DnaseI.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR PRINTS; PR00130; DNASEI.
DR PRODOM; PD005408; DnaseI; 1.
DR SMART; SM00476; DnaseIc; 1.
DR PROSITE; PS00919; DNASE_I_1; 1.
DR PROSITE; PS00918; DNASE_I_2; 1.
SQ SEQUENCE 284 AA; 32126 MW; 7382E20515EEAE11 CRC64;

Query Match 82.7%; Score 1131; DB 11; Length 284;
Best local similarity 81.9%; Pred. No. 5.1e-103;
Matches 213; Conservative 23; Mismatches 24; Indels 0; Gaps 0;
Qy 1 LKTAARNIQTFFGTSMNATLVSYIVQILSRVDIALVOEVRDLSHTAVGKLLDNLNDAP 60
-|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
Db 23 LRKTAARNIQTFFGTSMNATLVSYIVQILSRVDIALVOEVRDLSHTAVGKLLDNLNDAP 82
Qy 61 DTVHYVVSPLGRKSYKERYLFVFRPDQVSAVDVSYDDGCEPCGNDTFRPAIVRFFS 120


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Db 83 DTRYVVSSELRKSKYKQVLFYRDPQVSLDSYDQDCEPCGNDTFSREPAIVKFS 142
Qy 121 RFTVEVREFAIVLHAAPGDAVABIDALYDVLQVQKGLDVLMLGDFNAGCSYVRPSQ 180
Db 143 FYTEVQVREFAIVLHAAPGDAVABIDALYDVLQVQKGLDVLMLGDFNAGCSYVRPSQ 202
Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPCHAYDRIVVAGMLRGAVVPSALPFPQAAVG 240
Db 203 WSSIRLWTSPTFQWLIPDSADTTATPCHAYDRIVVAGMLRGAVVPSALPFPQAAVG 262
Qy 241 LSDQLAQAIISDHYPEVLMK 260
Db 263 LSNQLAEAIISDHYPEVTLR 282

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RESULT 2

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ID Q95KK2 PRELIMINARY; PRT; 284 AA.
AC Q95KK2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Deoxyribonuclease I.
GN DNASEI.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=21303096; PubMed=11410284;
RA Mori S., Yasuda T., Takeshita H., Nakajima T., Nakazato E., Mogi K.,
RA Kaneko Y., Kishi K.;
RT "Molecular, biochemical and immunological analyses of porcine
RL Biochim. Biophys. Acta 1547:275-287(2001).
DR EMBL; AB048832; BAB62268.1; -.
DR InterPro; IPR001582; DNase I.
DR Pfam; PF03372; Exo endo phos; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNaseI_1; 1.
DR SMART; SM00476; DNaseIc_1; 1.
DR PROSITE; PS00919; DNaseI_1; 1.
DR PROSITE; PS00918; DNaseI_2; 1.
SQ SEQUENCE 284 AA; 31625 MW; 1348C169B61EB8C9 CRC64;

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Query Match 80.4%; Score 1099; DB 6; Length 284;
Best Local Similarity 79.2%; Pred. No. 7.2e-100;
Matches 206; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

Qy 1 LKIAAFNIOTFGTGMNATLVSYVQILSRDYALVQEVDRSHLTAVGKLLDNLNQAP 60
Db 23 LRIAFAFNIRTFGTGMNATLVSYVQILSRDYALVQEVDRSHLTAVGKLLDNLNQDP 82
Qy 61 DTHYVVSSELRKSKYKQVLFYRDPQVSLDSYDQDCEPCGNDTFSREPAIVRFS 120
Db 83 NYHHVVSSELRKSKYKQVLFYRDPQVSLDSYDQDCEPCGNDTFSREPAIVRFS 142
Qy 121 RFTVEVREFAIVLHAAPGDAVABIDALYDVLQVQKGLDVLMLGDFNAGCSYVRPSQ 180
Db 143 PSTQVKEFAIVLHAAPGDAVABIDALYDVLQVQKGLDVLMLGDFNAGCSYVTTSH 202
Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPCHAYDRIVVAGMLRGAVVPSALPFPQAAVG 240
Db 203 WSSIRLWTSPTFQWLIPDSADTTATPCHAYDRIVVAGMLRGAVVPSALPFPQAAVG 262
Qy 241 LSDQLAQAIISDHYPEVLMK 260
Db 263 LSEQTALAIISDHYPEVTLK 282

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RESULT 3

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Q8K0U1 PRELIMINARY; PRT; 332 AA.
ID Q8K0U1;
AC Q8K0U1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to deoxyribonuclease I.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC030394; AAH30394.1; -.
DR InterPro; IPR001582; DNase I.
DR Pfam; PF03372; Exo endo phos; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNaseI_1; 1.
DR SMART; SM00476; DNaseIc_1; 1.
DR PROSITE; PS00919; DNaseI_1; 1.
DR PROSITE; PS00918; DNaseI_2; 1.
SQ SEQUENCE 332 AA; 37769 MW; 1A0B890E8512FB47 CRC64;

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Query Match 80.2%; Score 1097; DB 11; Length 332;
Best Local Similarity 69.2%; Pred. No. 1.4e-99;
Matches 213; Conservative 23; Mismatches 24; Indels 48; Gaps 1;

Qy 1 LKTAAFNIOTFGTGMNATLVSYVQILSRDYALVQEVDRSHLTAVGKLLDNLN---- 56
Db 23 LRIAFAFNIRTFGTGMNATLVSYVQILSRDYALVQEVDRSHLTAVGKLLDNLNRRWT 82
Qy 57 -----ODAPDTYHYVVSSEPLG 72
Db 83 VLESYSIMTTIYSLTPSVLYCWSPAIRCOEAPSMKLYLWFLPSRDKPTDYVYVVSSEPLG 142
Qy 73 RKSKYKRYLFVYRDPQVSAVDYDQDCEPCGNDTFSREPAIVRFSRETEVREFAIVP 132
Db 143 RKSKYKRYLFVYRDPQVSAVDYDQDCEPCGNDTFSREPAIVRFSRETEVREFAIVP 202
Qy 133 LHAAPGDAVABIDALYDVLQVQKGLDVLMLGDFNAGCSYVRPSQSSIRLWTSPTF 192
Db 203 LHAAPTEAVSEIDALYDVLQVQKGLDVLMLGDFNAGCSYVRPSQSSIRLWTSPTF 262
Qy 193 QWLIPDSADTTATPCHAYDRIVVAGMLRGAVVPSALPFPQAAVGLSOLAIAISDH 252
Db 263 QWLIPDSADTTATPCHAYDRIVVAGMLRGAVVPSALPFPQAAVGLSOLAIAISDH 322
Qy 253 YPVEVLMK 260
Db 323 YPVEVTLR 330

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RESULT 4

```

Q8MJ27 PRELIMINARY; PRT; 282 AA.
ID Q8MJ27;
AC Q8MJ27;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Deoxyribonuclease I precursor (EC 3.1.21.1).
GN DNASEI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP SEQUENCE FROM N.A.
RA De Maria A.B., Arruti C.;
RT "Bovine DNase I gene for deoxyribonuclease I.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528509; AAM93248.1; -.
DR InterPro; IPR001582; DNase I.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR PRINTS; PR00130; DNaseI.
DR ProDom; PD005408; DNase_I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR PROSITE; PS00919; DNase_I_1; 1.
DR PROSITE; PS00918; DNase_I_2; 1.
KW Signal; Hydrolase.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 282 AA; 31331 MW; 4385B810C00700E2 CRC64;

Query Match 77.8%; Score 1064; DB 6; Length 282;
Best Local Similarity 77.6%; Pred. No. 2e-96;
Matches 201; Conservative 29; Mismatches 29; Indels 0; Gaps 0;

QY 1 LKIAAFNIOTFGETKMSNATLVSYIVQLSRDYALVOEVRDLSHTAVGKLLDNLNODAP 60
DB 23 LKIAAFNIOTFGETKMSNATLVSYIVRRYDIQLQEVDSHLVAVGKLLDYLNDQDP 82
QY 61 DTHYVWSEPLGRKSYKERYLFVYRPPQVSAVDYVDDGCEPCGNDTFNREPAIVRFFS 120
DB 83 NTHYVWSEPLGRNSYKERYLFPRPKVSVLDYVDDGCEPCGNDTFNREPAIVRFFS 142
QY 121 RETEVRFAIVLHAAPGDAVAEIDALYDVLVDOEKWGLDVMGMDFNAGCSYVRPSQ 180
DB 143 HSTKVKKEFAIVLHSAAPSADVAEINSLYDVLVDOQKWLNDVLMGMDFNAGCSYVTSSQ 202
QY 181 WSSIRLWTSPTFQWLPDSDATTTATPHCAVDRIIVAGKLLRGAVVPSALPFRQAYG 240
DB 203 WSSIRLWTSPTFQWLPDSDATTTATSTNCAYDRIIVAGSLQSSVVPFQAYG 262
QY 241 LSDQLAQAIISDRYPVEVNL 259
DB 263 LSNEMALAIISDRYPVEVTL 281

RESULT 5
Q9GLG6 PRELIMINARY; PRT; 272 AA.
ID Q9GLG6
AC Q9GLG6; Q9GLG62;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Epithelial lens deoxyribonuclease I (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA De Maria A.B., Sanguinetti C.J., Arruti C.;
RT "DNase I in bovine epithelial lens cells.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF311922; AAG28792.2; -.
DR HSP; P00639; 3DNI.
DR InterPro; IPR001582; DNase I.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR PRINTS; PR00130; DNaseI.
DR ProDom; PD005408; DNase_I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR PROSITE; PS00919; DNase_I_1; 1.
DR PROSITE; PS00918; DNase_I_2; 1.
FT NON TER 1 1
SQ SEQUENCE 272 AA; 30179 MW; DE0B689E4D854446 CRC64;

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Query Match 77.5%; Score 1060; DB 6; Length 272;
Best Local Similarity 77.6%; Pred. No. 4.7e-96;
Matches 201; Conservative 28; Mismatches 30; Indels 0; Gaps 0;

QY 1 LKIAAFNIOTFGETKMSNATLVSYIVQLSRDYALVOEVRDLSHTAVGKLLDNLNODAP 60
DB 13 LKIAAFNIOTFGETKMSNATLVSYIVRRYDIQLQEVDSHLVAVGKLLDYLNDQDP 72
QY 61 DTHYVWSEPLGRKSYKERYLFVYRPPQVSAVDYVDDGCEPCGNDTFNREPAIVRFFS 120
DB 73 NTHYVWSEPLGRNSYKERYLFPRPKVSVLDYVDDGCEPCGNDTFNREPAIVRFFS 132
QY 121 RETEVRFAIVLHAAPGDAVAEIDALYDVLVDOEKWGLDVMGMDFNAGCSYVRPSQ 180
DB 133 HSTKVKKEFAIVLHSAAPSADVAEINSLYDVLVDOQKWLNDVLMGMDFNAGCSYVTSSQ 192
QY 181 WSSIRLWTSPTFQWLPDSDATTTATPHCAVDRIIVAGKLLRGAVVPSALPFRQAYG 240
DB 193 WSSIRLWTSPTFQWLPDSDATTTATSTNCAYDRIIVAGSLQSSVVPFQAYG 252
QY 241 LSDQLAQAIISDRYPVEVNL 259
DB 253 LSNEMALAIISDRYPVEVTL 271

RESULT 6
Q90YAA PRELIMINARY; PRT; 282 AA.
ID Q90YAA
AC Q90YAA;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE DNase I (Deoxyribonuclease I).
OS Elaphe quadrivirgata (Japanese four-lined ratsnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Colubridae; Colubrinae; Elaphe.
OC NCBI_TaxID=31143; 86195;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.elaphequadrivirgata; TISSUE=Pancreas;
RA Yasuda T.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.elaphequadrivirgata; TISSUE=Pancreas;
RA Yasuda T.;
RT "cDNA encoding Elaphe quadrivirgata pancreatic deoxyribonuclease I.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB058784; BAB68563.1; -.
DR EMBL; AB046545; BAB82990.1; -.
DR InterPro; IPR001582; DNase I.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR PRINTS; PR00130; DNaseI.
DR ProDom; PD005408; DNase_I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR PROSITE; PS00919; DNase_I_1; 1.
DR PROSITE; PS00918; DNase_I_2; 1.
SQ SEQUENCE 282 AA; 31267 MW; 0D0268192E9EB681 CRC64;

Query Match 58.8%; Score 804; DB 13; Length 282;
Best Local Similarity 58.5%; Pred. No. 8.4e-71;
Matches 152; Conservative 43; Mismatches 65; Indels 0; Gaps 0;

QY 1 LKIAAFNIOTFGETKMSNATLVSYIVQLSRDYALVOEVRDLSHTAVGKLLDNLNODAP 60
DB 21 LAIGAFNIRAFGDKLSNQTSSSIVRLITTYDLVLQEVDSHLVAVGKLLDYLNDQDP 80
QY 61 DTHYVWSEPLGRKSYKERYLFVYRPPQVSAVDYVDDGCEPCGNDTFNREPAIVRFFS 120

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Db      81 DPEGLYLSKPLGNSYKEQLFYVRQDRVSPVESYDDGCEPCGNGTFSREPFIVKFAV 140
Qy      121 RFTVEFEAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
Db      141 POAAVEELVLPLHAAPAAVTEIDSLDYQVQDKRWGVTDALLGDFNADCNVQAE 200
Qy      181 WSSIRLWTSPTFOWLIIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFFFOAAYG 240
Db      201 WPSIRLSKDFOWLIIPDADTTVTNTICAYDRIVVAGSKLRESILPATAKVDNFQKTLK 260
Qy      241 LSDQLAQASIDHYVPEVLMK 260
Db      261 LSSKDALAVSDHPPVEVTLK 280

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RESULT 7

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Q8UWB6 Q8UWB6 PRELIMINARY; PRT; 282 AA.
AC Q8UWB6;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Deoxyribonuclease I.
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasuda T.;
RT "cDNA encoding Agkistrodon halys pancreatic deoxyribonuclease I.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB050701; BAB82523.1; -.
DR InterPro; IPR001582; DNase I.
DR InterPro; IPR005135; Exo endo phos.
DR Pfam; PF03372; Exo endo phos; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNase_I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR PROSITE; PS00919; DNASE_I_1; 1.
SQ SEQUENCE 282 AA; 31569 MW; 4843884A40332366 CRC64;

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Query Match 56.6%; Score 801; DB 13; Length 282;
 Best Local Similarity 58.5%; Pred. No. 1.7e-70;
 Matches 152; Conservative 43; Mismatches 65; Indels 0; Gaps 0;

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Qy      1 LKTAAPNIQTGCTKMSNATLVSYIVQILSRDYDALVQVRDLSHTAVGKLLDNLNQDAP 60
Db      21 LRIGAFNIRAFGDKLSNQTSISFIVRLTAYDALIQVRDADLSAVKLMHLVNWASP 80
Qy      61 DTHYVYSEPLGRKSKERYLFVVRPDQVSAVDYVYDDGCEPCGNDTFNREPAIVRFFS 120
Db      81 NAFSILVSKPLGNSHKEQLFYVRDRVSPVESYDDGCEPCGNTFSRAFFIVKFAV 140
Qy      121 RFTVEFEAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
Db      141 POAAVEELVLPLHAAPAAVTEIDSLDYQVQDKRWGVTDALLGDFNADCNVQAE 200
Qy      181 WSSIRLWTSPTFOWLIIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFFFOAAYG 240
Db      201 WPSIRLSKDFOWLIIPDADTTVTNTICAYDRIVVAGSKLRESILPATAKVDNFQKTLK 260
Qy      241 LSDQLAQASIDHYVPEVLMK 260
Db      261 LSSKDALAVSDHPPVEVILK 280

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RESULT 8

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Q9PTY8 Q9PTY8 PRELIMINARY; PRT; 283 AA.
ID Q9PTY8
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AC Q9PTY8;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Deoxyribonuclease I.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakashima Y., Yasuda T., Takeshita H., Nakajima T., Hosomi O.,
RA Mori S., Kishi K.;
RT Molecular, biochemical and immunological studies of hen pancreatic
RT deoxyribonuclease I.;
RL Int. J. Biochem. Cell Biol. 31:1315-1326(1999).
DR EMBL; AB013751; BAA88714.1; -.
DR HSSP; P00639; 3DNI.
DR InterPro; IPR001582; DNase I.
DR InterPro; IPR005135; Exo endo phos.
DR Pfam; PF03372; Exo endo phos; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNase_I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR PROSITE; PS00918; DNASE_I_2; 1.
SQ SEQUENCE 283 AA; 31495 MW; E5B2596E33DFC600 CRC64;

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Query Match 55.5%; Score 759; DB 13; Length 283;
 Best Local Similarity 58.1%; Pred. No. 2.3e-66;
 Matches 151; Conservative 34; Mismatches 75; Indels 0; Gaps 0;

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Qy      1 LKTAAPNIQTGCTKMSNATLVSYIVQILSRDYDALVQVRDLSHTAVGKLLDNLNQDAP 60
Db      22 LRISAFNIQTGDSKMSNOTVAGFIVSILVQYDITLVQVDRDADLSVVKLVQSLNSASS 81
Qy      61 DTHYVYSEPLGRKSKERYLFVVRPDQVSAVDYVYDDGCEPCGNDTFNREPAIVRFFS 120
Db      82 YPYSFLSSIPLGNSYKEQYFVRSDIVSVLESYVYDDGCEPCGTDIFSREPFIVKFAV 141
Qy      121 RFTVEFEAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
Db      142 PTTQLDFVIVPLHAAPAAVTEIDSLDYQVQDKRWGVTDALLGDFNADCNVQAE 201
Qy      181 WSSIRLWTSPTFOWLIIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFFFOAAYG 240
Db      202 WPSIRLSKSCENILIPDSADTTVTSTDCAYDRIVVAGSALRQAVEYGSATVDNFQETLH 261
Qy      241 LSDQLAQASIDHYVPEVLMK 260
Db      262 IQNKDALAISDHPPEVETLK 281

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RESULT 9

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Q8UJP7 Q8UJP7 PRELIMINARY; PRT; 279 AA.
ID Q8UJP7
AC Q8UJP7;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE DNase I.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Mogi K.;
RT "Carp DNase I.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; AB075779; BAC00811.1; --
DR InterPro; IPR001582; DNase I.
DR InterPro; IPR005135; Exo endo phos.
DR Pfam; PF03372; Exo endo phos; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNase I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR PROSITE; PS00919; DNase I; 1.
DR PROSITE; PS00918; DNase I; 2; 1.
SQ SEQUENCE 279 AA; 30983 MW; 570F758851A2AB6 CRC64;

Query Match 54.7%; Score 748; DB 13; Length 279;
Best Local Similarity 55.4%; Pred. No. 2.7e-65;
Matches 144; Conservative 40; Mismatches 74; Indels 2; Gaps 2;

QY 1 LKIAAFNIQFGETKMSNATLVSVIQLSRYSYDIALVQVDSHLTAVGKLLDNLN-QDA 59
DB 20 LLGAFNIKFGDSKASNATLDDITIKVHRHYDIVLIQVDSHLDLTATNKLMSQVNGSS 79
QY 60 PUYHYVVSPLGRKSKYKERYLFVYRPDQVSAVDSYDDGCEPCGNDTFNREPAIVRF 119
DB 80 PYEQYIVSEPLGRKSKYKERYLFYRRQAVSVANSFYDDGCEGCTGTFNREPFVWFS 139
QY 120 SRFTVEFEFAIVPLHAPGDAVAEIDALYDVLDVQEKWGLDVMLGDFNAGCSYVRS 179
DB 140 SNTAVQKFAIVPQRTSPVAVTEIDALHDVLDLTQRUNTNMILGDFNAGCSYVNS 199
QY 180 QWSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIYVAGMLRGAVPDSALPFNFQAY 239
DB 200 DMSKRLRTDQSYTLIPDSADTTVTHTNGPYDRIYVATSDMMKG-VSAGSAQVDFMQAH 258
QY 240 GLSDQLAQAISSHYVPEVWL 259
DB 259 GLSQSLWGLVSDHFFAEVQL 278

RESULT 10
Q9D1G0 PRELIMINARY; PRT; 278 AA.
ID Q9D1G0
AC Q9D1G0
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE 4733401H14RIK protein.
GN 4733401H14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

DR EMBL; AK003619; BAB22893.1; --
DR HSSP; P00639; 2DNJ
DR MGD; MGI:191355; 4733401H14RIK.
DR InterPro; IPR001582; DNase I.
DR InterPro; IPR005135; Exo endo phos.
DR Pfam; PF03372; Exo endo phos; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNase I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR PROSITE; PS00919; DNase I; 1.
DR PROSITE; PS00918; DNase I; 2; 1.
SQ SEQUENCE 278 AA; 31138 MW; 71FEA07A1BF940E8 CRC64;

Query Match 50.8%; Score 694.5; DB 11; Length 278;
Best Local Similarity 53.5%; Pred. No. 5.1e-60;
Matches 139; Conservative 36; Mismatches 80; Indels 5; Gaps 1;

QY 1 LKIAAFNIQFGETKMSNATLVSVIQLSRYSYDIALVQVDSHLTAVGKLLDNLNQDA 60
DB 22 LRIGAFNVQSGDNKVSOPDCGVIQAQLAGIDIALVQVDRDPLSAVSLMEQINRVSK 81
QY 61 DTHYVVSPLGRKSKYKERYLFVYRPDQVSAVDSYDDGCEPCGNDTFNREPAIVRF 120
DB 82 HEYGFVSSPLGRKSKYKERYLFVYRPDQVSAVDSYDDGCEPCGNDTFNREPAIVRF 136
QY 121 RFTVEFEFAIVPLHAPGDAVAEIDALYDVLDVQEKWGLDVMLGDFNAGCSYVRS 180
DB 137 FSCATKELVLIPLHAPGDAVAEIDALYDVLDVQEKWGLDVMLGDFNAGCSYVRS 196
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIYVAGMLRGAVPDSALPFNFQAY 240
DB 197 WPSIRLRSSEVFKWLPDSADTTVGNDSQCAVDRIYVAGMLRSLKPHSASVHNFQEF 256
QY 241 LSLDLAQAISSHYVPEVWL 260
DB 257 LDTQALASDHFFAEVTEK 276

RESULT 11
Q9D645 PRELIMINARY; PRT; 278 AA.
ID Q9D645
AC Q9D645
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE 4733401H14RIK protein.
GN 4733401H14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

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RL Nature 409:685-690(2001).
DR EMBL: AK014633; BAB29476.1; -.
DR HSP; P00639; 2DNJ.
DR MGD; MGI:1913955; 4733401H14R1K.
DR InterPro; IPR001582; DNase_I.
DR Pfam; P003372; Exo_endo_phos.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNase_I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR PROSITE; PS00919; DNASE_I_1; 1.
SQ SEQUENCE 278 AA; 31206 MW; 10734C10DD5F5EC6C CRC64;

Query Match 49.6%; Score 678.5; DB 11; Length 278;
Best Local Similarity 52.7%; Pred. No. 1.9e-58;
Matches 137; Conservative 36; Mismatches 82; Indels 5; Gaps 1;

QY 1 LKIAAPNIOTFGTQKSNATLVSYIVQILSRDYDIALVOEVRDLSHTAVGKLLDNLNQDAP 60
DB 22 LAIGAFNVQSGDKVSDPDGCVIAQTLAGYDIALVOEVRDPLSAVSLMLQINRVSK 81
QY 61 DTYHYVVSPELGRKSKYKERYLFVYRPDQVSAVDYVYDDGCEPCGNDTFNREPAIVRFFS 120
DB 82 HEYGFVSSPELGRKSKYKERYLFVYRPDQVSAVDYVYDDGCEPCGNDTFNREPAIVRFFS 136
QY 121 RTEVREPAIVPLHAAPGDAVAEIDALYDVYDVOEKMGLEDVLMGDFNAGCSYVRPSQ 180
DB 137 PSCATKELVLIPLHAAPGDAVAEIDALYDVYDVOEKMGLEDVLMGDFNAGCSYVRPSQ 196
QY 181 WSIRLWTSPTQWLIPQSDATTATPTHCAYDRIIVAGMLLGAAGVVPDSALPFNFQAYG 240
DB 197 WFSIRLSSEVEFKWLPIDSAHTTGVNSDCAYDRIIVAGMLLGAAGVVPDSALPFNFQAYG 256
QY 241 LSDQLAQAISSHYVPEVMLK 260
DB 257 LPQTQALASDHFVEVETK 276

RESULT 12
Q90WM1 PRELIMINARY; PRT; 353 AA.
AC Q90WM1 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Deoxyribonuclease I.
GN DNASEI
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21332560; PubMed=11439097;
RA Takeshita H., Yasuda T., Iida R., Nakajima T., Mori S., Mogi K.,
RA Kaneko Y., Kishi K.;
RT "Amphibian DNases I are characterized by a C-terminal end with a
RT unique cysteine-rich stretch and by the insertion of a serine residue
RT into a Ca2+-binding site."
RL Biochem. J. 357:473-480(2001).
DR EMBL; AB038776; BAB62088.1; -.
DR InterPro; IPR001582; DNase_I.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR001212; Somatomedin_B.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR Pfam; PF01033; Somatomedin_B; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNase_I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR InterPro; IPR001582; DNase_I.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR001212; Somatomedin_B.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR Pfam; PF01033; Somatomedin_B; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNase_I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR SMART; SM00201; SO; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; 1.
SQ SEQUENCE 353 AA; 39192 MW; F7AFC30AB05B607A CRC64;

Query Match 48.8%; Score 666.5; DB 13; Length 353;
Best Local Similarity 46.4%; Pred. No. 4.1e-57;
Matches 121; Conservative 61; Mismatches 78; Indels 1; Gaps 1;

QY 1 LKIAAPNIOTFGTQKSNATLVSYIVQILSRDYDIALVOEVRDLSHTAVGKLLDNLNQDAP 60
DB 20 LKIASFNTERFATKVDVPPVNLRLIQLRRYELIAVQEVMSKNTAIRLVLQELNATG 79
QY 61 DTYHYVVSPELGRKSKYKERYLFVYRPDQVSAVDYVYDDGCEPCGNDTFNREPAIVRFFS 120
DB 80 LHYNLLISDHLGRSSYREKYVYIREDILKPTWYHYDDGCGCTGVFIREPFVAFSS 139

Q90WM0 PRELIMINARY; PRT; 353 AA.
AC Q90WM0 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Deoxyribonuclease I.
GN DNASEI
OS Bufo japonicus (Japanese toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae; Bufo.
OX NCBI_TaxID=8387;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21332560; PubMed=11439097;
RA Takeshita H., Yasuda T., Iida R., Nakajima T., Mori S., Mogi K.,
RA Kaneko Y., Kishi K.;
RT "Amphibian DNases I are characterized by a C-terminal end with a
RT unique cysteine-rich stretch and by the insertion of a serine residue
RT into a Ca2+-binding site."
RL Biochem. J. 357:473-480(2001).
DR EMBL; AB045037; BAB62090.1; -.
DR InterPro; IPR001582; DNase_I.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR001212; Somatomedin_B.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR Pfam; PF01033; Somatomedin_B; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNase_I; 1.
DR SMART; SM00476; DNaseIc; 1.
DR SMART; SM00201; SO; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; 1.
SQ CHAIN 20 353 DEOXYRIBONUCLEASE I.
SQ SEQUENCE 353 AA; 39295 MW; 761BEE288724AB5C CRC64;

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QY 121 RFEVREFAIPLHAAPGDAVAEIDALDYVLDVQEKWGLDVMMLGDFNAGCSYVRPSQ 180
Db 140 LTELKDFALVSIHTSPYAVREVGLVWEDAKQRLLEDILILGDYNGAGCSYVKTSH 199
QY 181 WSSIRLWTSPTFOWLPDSADTT-ATPHTCAYDRIVVAGMLRGAIVVPSALPFRNQAY 239
Db 200 WPNIRLQSSLOWLIGDTEGSTVNTNCPYDRVLVGGARFQDTVIPGTAKAFNYHAY 259
QY 240 GLSDQLAQAISSDHYVVEVMLK 260
Db 260 DLTYEMAKAVSDHYVVEVMEIR 280

RESULT 14
Q9DEG8 PRELIMINARY; PRT; 350 AA.
AC Q9DEG8:
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE deoxyribonuclease I.
GN DNASEI.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SQ SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Hosomi O., Yasuda T., Takeshita H., Nakajima T., Nakashima Y.,
RA Mori S., Mogi K., Hanaoka Y., Kishi K.;
RT "Molecular cloning of cDNA encoding Xenopus laevis deoxyribonuclease
RT I.";
RL DNA Seq. 11:247-255 (2000).
DR EMBL; AB030958; BAB20384.1; -.
DR HSSP; P00639; 3DN1.
DR InterPro; IPR001582; DNaseI.
DR InterPro; IPR005135; Exo endo phos.
DR Pfam; PF03372; Somatomedin_B.
DR Pfam; PF01033; Somatomedin_B; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNaseI; 1.
DR SMART; SM00476; DNaseIc; 1.
DR SMART; SM00201; SO; 1.
SQ SEQUENCE 350 AA; 39265 MW; 7CB66AFC91BCE70 CRC64;

Query Match 46.0%; Score 628.5; DB 13; Length 350;
Best Local Similarity 44.8%; Pred. No. 2.2e-53;
Matches 116; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 2 KIAAFNIQTGCTGMSNATLVSYVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQAPD 61
Db 21 KIAAFNIQTGCTGMSNATLVSYVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQAPD 61
QY 62 TYHYVVSSEPLGRKSYKERYLVYRDPQVSAVDVYDDGCEPCGNDTFNREPAPFR 121
Db 81 NYNVLSLHGRSSYREKAYVIREIVPTWYHFDGCEPCGNDTFNREPAPFR 140
QY 122 FTEVREFAIPLHAAPGDAVAEIDALDYVLDVQEKWGLDVMMLGDFNAGCSYVRPSQ 181
Db 141 TTVVKDFALISHTSPYAVREVGLVWEDAKQRLLEDILILGDYNGAGCSYVKTSH 199
QY 182 SSIRLWTSPTFOWLPDSADTT-ATPHTCAYDRIVVAGMLRGAIVVPSALPFRNQAY 240
Db 201 PIIRLHREBELWLGIXEETTVSNTNCPYDRVLVGGARFQDTVIPGTAKAFNYHAY 259
QY 241 LSDQLAQAISSDHYVVEVML 260
Db 261 LTTEMKAVSDHYVVEVMEIR 280

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RESULT 15

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Q9YI04 PRELIMINARY; PRT; 295 AA.
AC Q9YI04:
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE deoxyribonuclease gamma.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SQ SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Shiohawa D., Tanuma S.;
RT "cDNA cloning of Xenopus DNase gamma.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF059612; AAC64266.1; -.
DR HSSP; P00639; 2DNJ.
DR InterPro; IPR001582; DNaseI.
DR InterPro; IPR005135; Exo endo phos.
DR Pfam; PF03372; Exo endo phos; 1.
DR PRINTS; PR00130; DNASEI.
DR ProDom; PD005408; DNaseI; 1.
DR SMART; SM00476; DNaseIc; 1.
DR SMART; SM00201; SO; 1.
SQ SEQUENCE 295 AA; 34223 MW; B185C7FCFF1A6C80 CRC64;

Query Match 45.9%; Score 628; DB 13; Length 295;
Best Local Similarity 47.9%; Pred. No. 2e-53;
Matches 126; Conservative 47; Mismatches 86; Indels 4; Gaps 3;

QY 1 LXIAAFNIQTGCTGMSNATLVSYVQILSRDYIALVQEVDRDHLTAVGKLLDNLN--QD 58
Db 18 LRICSFNVQSGESKRDKPAVMNVVVKIISRCITLLMEIKDSSNTVIRLMAQLNSQE 77
QY 59 APDTYHYVVSSEPLGRKSYKERYLVYRDPQVSAVDVYDDGCEPCGNDTFNREPAPFR 118
Db 78 TRNQFDLITISQRLGRKSYKERYLVYRDPQVSAVDVYDDGCEPCGNDTFNREPAPFR 136
QY 119 FSRFTEVREFAIPLHAAPGDAVAEIDALDYVLDVQEKWGLDVMMLGDFNAGCSYVRP 178
Db 137 QAPSTEVEKEFVIVPQHTTPEAAVREIDELDYVLDVQEKWGLDVMMLGDFNAGCSYVRP 196
QY 179 SOWSIRLWTSPTFOWLPDSADTTA-TPTHCAYDRIVVAGMLRGAIVVPSALPFRNQ 237
Db 197 KSWKIRLKNHTFVWLGIDNDITVKSSTNCATDRIVVVGKLVSSIVPGSANVDFMV 256
QY 238 AYGLSDQLAQAISSDHYVVEVMLK 260
Db 257 AYGLTEEQALEVSDHFFIEVRLK 279

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Search completed: November 21, 2003, 13:56:34
 Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 13:46:51; Search time 21 Seconds

(without alignments)
523.849 Million cell updates/sec

Title: US-10-005-306-9

Perfect score: 1367

Sequence: 1 LKIAAFNIQTGTGKMSNAT.....LSQDLAQAISEHVPVEMLK 260

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1367	100.0	260	4 US-08-663-831-9	Sequence 9, Appli
2	1364	99.8	260	4 US-08-663-831-10	Sequence 10, Appli
3	1362	99.6	260	4 US-09-796-774-1	Sequence 1, Appli
4	1362	99.6	260	4 US-08-663-831-1	Sequence 1, Appli
5	1362	99.6	260	4 US-08-663-831-14	Sequence 14, Appli
6	1362	99.6	260	4 US-10-074-509-4	Sequence 4, Appli
7	1362	99.6	346	1 US-07-895-300A-1	Sequence 1, Appli
8	1362	99.6	346	4 US-09-638-112-1	Sequence 1, Appli
9	1362	99.6	346	5 PCT-US93-05136-1	Sequence 1, Appli
10	1358	99.3	260	4 US-08-663-831-2	Sequence 2, Appli
11	1358	99.3	260	4 US-08-663-831-3	Sequence 3, Appli
12	1358	99.3	260	4 US-08-663-831-11	Sequence 11, Appli
13	1358	99.3	260	4 US-08-663-831-15	Sequence 15, Appli
14	1357	99.3	260	4 US-08-663-831-4	Sequence 4, Appli
15	1357	99.2	346	1 US-08-458-367-1	Sequence 1, Appli
16	1356	99.2	260	4 US-08-663-831-5	Sequence 5, Appli
17	1356	99.2	260	4 US-08-663-831-6	Sequence 6, Appli
18	1356	99.2	260	4 US-08-663-831-12	Sequence 12, Appli
19	1356	99.2	260	4 US-08-663-831-13	Sequence 13, Appli
20	1356	99.2	260	4 US-08-663-831-16	Sequence 16, Appli
21	1354	99.0	260	4 US-08-663-831-8	Sequence 8, Appli
22	1353	99.0	260	4 US-08-663-831-7	Sequence 7, Appli
23	1352	98.9	260	4 US-08-663-831-17	Sequence 17, Appli
24	592	43.3	310	2 US-08-640-745A-1	Sequence 1, Appli
25	592	43.3	310	3 US-09-073-633-1	Sequence 3, Appli
26	591	43.2	285	4 US-10-074-509-3	Sequence 3, Appli
27	591	43.2	305	4 US-10-074-509-2	Sequence 2, Appli

28 463.5 33.9 302 4 US-09-662-746A-2 Sequence 2, Appli
29 461.5 33.8 351 2 US-08-468-012A-2 Sequence 2, Appli
30 461.5 33.8 351 3 US-09-054-989-2 Sequence 2, Appli
31 454 33.2 113 3 US-08-406-030A-29 Sequence 29, Appli
32 193 14.1 38 1 US-07-895-300A-17 Sequence 17, Appli
33 193 14.1 38 1 US-08-458-367-17 Sequence 17, Appli
34 193 14.1 38 5 PCT-US93-05136-17 Sequence 17, Appli
35 193 14.1 38 5 PCT-US93-05136-17 Sequence 17, Appli
36 186 13.6 32 1 US-08-458-367-9 Sequence 9, Appli
37 186 13.6 32 1 US-09-638-112-9 Sequence 9, Appli
38 186 13.6 32 5 PCT-US93-05136-9 Sequence 9, Appli
39 186 13.6 32 1 US-07-895-300A-15 Sequence 15, Appli
40 183 11.9 28 1 US-08-458-367-15 Sequence 15, Appli
41 163 11.9 28 5 PCT-US93-05136-15 Sequence 15, Appli
42 163 11.9 28 5 PCT-US93-05136-15 Sequence 15, Appli
43 163 11.9 28 1 US-07-895-300A-14 Sequence 14, Appli
44 157 11.5 28 1 US-08-458-367-14 Sequence 14, Appli
45 157 11.5 28 1 US-08-458-367-14 Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-08-663-831-9
; Sequence 9, Application US/08663831
; Patent No. 6331607
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,831
; FILING DATE: 14-Jun-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3562
; TELEFAX: 415/352-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-663-831-9

Query Match 100.0%; Score 1367; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 3.6e-151;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGTGKMSNATLVSYVQLSRDYALVOEVDLSHTAVGKLLDNLDAP 60
DB 1 LKIAAFNIQTGTGKMSNATLVSYVQLSRDYALVOEVDLSHTAVGKLLDNLDAP 60
QY 61 DTHYVWSEPLGRKSKERYLFVVRPDQVSAVDYVDDGCEPCGNDTFNRPAIVRFFS 120
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Db 61 DTHYVVSPLGRKSKERYLFFVYRPDQVSAVDSYDDGCEPCGNDTFNREPAIVRFS 120
Qy 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMMLGDFNAGCSYVRPSQ 180
Db 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMMLGDFNAGCSYVRPSQ 180
Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPTTHCAYDRIVVAGMLLRGAVVPDSALPFFNFOAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTTHCAYDRIVVAGMLLRGAVVPDSALPFFNFOAYG 240
Qy 241 LSDQLAQAISSDHYEVEVMLK 260
Db 241 LSDQLAQAISSDHYEVEVMLK 260

RESULT 2

US-08-663-831-10
; Sequence 10, Application US/08663831
; Patent No. 6391607
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Pan, Clark Qun
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,831
; FILING DATE: 14-Jun-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-663-831-10

Query Match 99.8%; Score 1364; DB 4; Length 260;
Best Local Similarity 99.6%; Pred. No. 8e-151; 0; Indels 0; Gaps 0;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db 1 LKTAENIQTGFTKMSNATLVSYIVQLSRDYALVQEVDRSHLTAVGKLLDNLNDAP 60
Qy 61 DTHYVVSPLGRKSKERYLFFVYRPDQVSAVDSYDDGCEPCGNDTFNREPAIVRFS 120
Db 61 DTHYVVSPLGRKSKERYLFFVYRPDQVSAVDSYDDGCEPCGNDTFNREPAIVRFS 120
Qy 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMMLGDFNAGCSYVRPSQ 180
Db 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMMLGDFNAGCSYVRPSQ 180
Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPTTHCAYDRIVVAGMLLRGAVVPDSALPFFNFOAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTTHCAYDRIVVAGMLLRGAVVPDSALPFFNFOAYG 240

Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTTHCAYDRIVVAGMLLRGAVVPDSALPFFNFOAYG 240
Qy 241 LSDQLAQAISSDHYEVEVMLK 260
Db 241 LSDQLAQAISSDHYEVEVMLK 260

RESULT 3

US-09-796-774-1
; Sequence 1, Application US/09796774
; Patent No. 6348343
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Shak, Steven
; APPLICANT: Ulmer, Jana S.
; TITLE OF INVENTION: HUMAN DNASE I VARIANTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/796,774
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/929995
; FILING DATE: 15-SEP-1997
; APPLICATION NUMBER: 08/540527
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: 08/403873
; FILING DATE: 24-MAR-1995
; APPLICATION NUMBER: PCT/US95/02366
; FILING DATE: 24-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P0925PIC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3562
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-796-774-1

Query Match 99.6%; Score 1362; DB 4; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.4e-150;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LKTAENIQTGFTKMSNATLVSYIVQLSRDYALVQEVDRSHLTAVGKLLDNLNDAP 60
Db 1 LKTAENIQTGFTKMSNATLVSYIVQLSRDYALVQEVDRSHLTAVGKLLDNLNDAP 60
Qy 61 DTHYVVSPLGRKSKERYLFFVYRPDQVSAVDSYDDGCEPCGNDTFNREPAIVRFS 120
Db 61 DTHYVVSPLGRKSKERYLFFVYRPDQVSAVDSYDDGCEPCGNDTFNREPAIVRFS 120
Qy 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMMLGDFNAGCSYVRPSQ 180
Db 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMMLGDFNAGCSYVRPSQ 180

QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLRGAVVPDSALPFPFOAAYG 240
 Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLRGAVVPDSALPFPFOAAYG 240
 QY 241 LSDQLAQAIISDHYPEVVMK 260
 Db 241 LSDQLAQAIISDHYPEVVMK 260

RESULT 4

US-08-663-831-1
 ; Sequence 1, Application US/08663831
 ; Patent No. 6391607
 ; GENERAL INFORMATION:
 ; APPLICANT: Lazarus, Robert A.
 ; APPLICANT: Pan, Clark Qun
 ; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/663,831
 FILING DATE: 14-Jun-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Johnston, Sean A.
 REGISTRATION NUMBER: 35,910
 REFERENCE/DOCKET NUMBER: P1042
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-3562
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 260 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-08-663-831-1

Query Match 99.6%; Score 1362; DB 4; Length 260;
 Best Local Similarity 99.6%; Pred. No. 1.4e-150;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDLSHTAVGKLLDNLNQDAP 60
 Db 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDLSHTAVGKLLDNLNQDAP 60
 QY 61 DTHYVWSEPLGRKSKYKERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120
 Db 61 DTHYVWSEPLGRKSKYKERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120
 QY 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGDFNAGCSYVRPSQ 180
 Db 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGDFNAGCSYVRPSQ 180
 QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLRGAVVPDSALPFPFOAAYG 240
 Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLRGAVVPDSALPFPFOAAYG 240
 QY 241 LSDQLAQAIISDHYPEVVMK 260
 Db 241 LSDQLAQAIISDHYPEVVMK 260

RESULT 5

US-08-663-831-14
 ; Sequence 14, Application US/08663831
 ; Patent No. 6391607
 ; GENERAL INFORMATION:
 ; APPLICANT: Lazarus, Robert A.
 ; APPLICANT: Pan, Clark Qun
 ; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/663,831
 FILING DATE: 14-Jun-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Johnston, Sean A.
 REGISTRATION NUMBER: 35,910
 REFERENCE/DOCKET NUMBER: P1042
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-3562
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 260 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-08-663-831-14

Query Match 99.6%; Score 1362; DB 4; Length 260;
 Best Local Similarity 99.6%; Pred. No. 1.4e-150;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDLSHTAVGKLLDNLNQDAP 60
 Db 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDLSHTAVGKLLDNLNQDAP 60
 QY 61 DTHYVWSEPLGRKSKYKERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120
 Db 61 DTHYVWSEPLGRKSKYKERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120
 QY 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGDFNAGCSYVRPSQ 180
 Db 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGDFNAGCSYVRPSQ 180
 QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLRGAVVPDSALPFPFOAAYG 240
 Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLLRGAVVPDSALPFPFOAAYG 240
 QY 241 LSDQLAQAIISDHYPEVVMK 260
 Db 241 LSDQLAQAIISDHYPEVVMK 260

RESULT 6

US-10-074-509-4
 ; Sequence 4, Application US/10074509
 ; Patent No. 6482626
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.

```

;
;      Barton, Will F.
;
; TITLE OF INVENTION: HUMAN DNASE
;
; NUMBER OF SEQUENCES: 11
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Genentech, Inc.
;
; STREET: 1 DNA Way
;
; CITY: South San Francisco
;
; STATE: California
;
; COUNTRY: USA
;
; ZIP: 94080
;
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/10/074,509
;
; FILING DATE: 11-Feb-2002
;
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: 09/643,520
;
; FILING DATE: 22/08/2000
;
; APPLICATION NUMBER: 08/794827
;
; FILING DATE: 04-Feb-1997
;
; APPLICATION NUMBER: 60/109796
;
; FILING DATE: 05-Feb-1996
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Johnston, Sean A.
;
; REGISTRATION NUMBER: 35,910
;
; REFERENCE/DOCKET NUMBER: P1000R1C2
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 650/225-3562
;
; TELEFAX: 650/952-9891
;
; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 260 amino acids
;
; TYPE: Amino Acid
;
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
;
US-10-074-509-4

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Query Match          99.6%; Score 1362; DB 4; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.4e-150;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKTAAFNIQTGFTKMSNATLVSVIQLSRVDIALVQVDRSHLTAVGKLDNLNQDAP 60
Db 1 LKTAAFNIQTGFTKMSNATLVSVIQLSRVDIALVQVDRSHLTAVGKLDNLNQDAP 60

Qy 61 DTHYVVSSEPLGRKSKERYLFVVRPDQVSAVDYDDGCEPCGNDTNRREPAIVRFFS 120
Db 61 DTHYVVSSEPLGRKSKERYLFVVRPDQVSAVDYDDGCEPCGNDTNRREPAIVRFFS 120

Qy 121 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVDVQEKWGLDVLMLGDFNAGCSYVRPSQ 180
Db 121 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVDVQEKWGLDVLMLGDFNAGCSYVRPSQ 180

Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAAYG 240

Qy 241 LSDQLAQAI SDHYPEVWLK 260
Db 241 LSDQLAQAI SDHYPEVWLK 260

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RESULT 7
US-07-895-300A-1
; Sequence 1, Application US/07895300A
; Patent No. 5279823
; GENERAL INFORMATION:
; APPLICANT: Frenz, John
; APPLICANT: Shire, Steven J.

```

```

;
;      Sliwowski, Mary B.
;
; TITLE OF INVENTION: PURIFIED FORMS OF DNase
;
; NUMBER OF SEQUENCES: 17
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Genentech, Inc.
;
; STREET: 460 Point San Bruno Blvd
;
; CITY: South San Francisco
;
; STATE: California
;
; COUNTRY: USA
;
; ZIP: 94080
;
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: patin (Genentech)
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/07/895,300A
;
; FILING DATE: 19920608
;
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER:
;
; FILING DATE:
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Hensley, Max D.
;
; REGISTRATION NUMBER: 27,043
;
; REFERENCE/DOCKET NUMBER: 747
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 415/225-1994
;
; TELEFAX: 415/952-9881
;
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 346 amino acids
;
; TYPE: AMINO ACID
;
; TOPOLOGY: linear
;
US-07-895-300A-1

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Query Match          99.6%; Score 1362; DB 1; Length 346;
Best Local Similarity 99.6%; Pred. No. 2.1e-150;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKTAAFNIQTGFTKMSNATLVSVIQLSRVDIALVQVDRSHLTAVGKLDNLNQDAP 60
Db 76 LKTAAFNIQTGFTKMSNATLVSVIQLSRVDIALVQVDRSHLTAVGKLDNLNQDAP 135

Qy 61 DTHYVVSSEPLGRKSKERYLFVVRPDQVSAVDYDDGCEPCGNDTNRREPAIVRFFS 120
Db 136 DTHYVVSSEPLGRKSKERYLFVVRPDQVSAVDYDDGCEPCGNDTNRREPAIVRFFS 195

Qy 121 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVDVQEKWGLDVLMLGDFNAGCSYVRPSQ 180
Db 196 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVDVQEKWGLDVLMLGDFNAGCSYVRPSQ 255

Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAAYG 240
Db 256 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAAYG 315

Qy 241 LSDQLAQAI SDHYPEVWLK 260
Db 316 LSDQLAQAI SDHYPEVWLK 335

```

```

RESULT 8
US-09-638-112-1
; Sequence 1, Application US/09638112
; Patent No. 6440412
; GENERAL INFORMATION:
; APPLICANT: Frenz, John
; APPLICANT: Shire, Steven J.
; APPLICANT: Sliwowski, Mary B.
; TITLE OF INVENTION: PURIFIED FORMS OF DNase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,112
FILING DATE: 09-Aug-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/942561
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: P0747C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3562
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-638-112-1

Query Match 99.6%; Score 1362; DB 4; Length 346;
Best Local Similarity 99.6%; Pred. No. 2.1e-150;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGETKMSNATLSYIVQILSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
DB 76 LKIAAFNIQTGETKMSNATLSYIVQILSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 135
QY 61 DTHYVVSEPLGRKSKYERLFPYRPDQVSADVSYDDGCEPCGNDTFRREPAIVRFS 120
DB 136 DTHYVVSEPLGRKSKYERLFPYRPDQVSADVSYDDGCEPCGNDTFRREPAIVRFS 195
QY 121 RFTVEFEAIVPLHAAPGDAVAEIDALYDVLVQEKWGLDVMLMGDFNAGCSYVRPSQ 180
DB 196 RFTVEFEAIVPLHAAPGDAVAEIDALYDVLVQEKWGLDVMLMGDFNAGCSYVRPSQ 255
QY 181 WSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPSALPFFNQAYG 240
DB 256 WSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPSALPFFNQAYG 315
QY 241 LSDQLAQALSDHYFVVEVMLK 260
DB 316 LSDQLAQALSDHYFVVEVMLK 335

RESULT 9
PCT-US93-05136-1
Sequence 1, Application PC/TUS9305136
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05136
FILING DATE: 19930528
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 747PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US93-05136-1

Query Match 99.6%; Score 1362; DB 5; Length 346;
Best Local Similarity 99.6%; Pred. No. 2.1e-150;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGETKMSNATLSYIVQILSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 60
DB 76 LKIAAFNIQTGETKMSNATLSYIVQILSRDYDIALVQEVDRSHLTAVGKLLDNLNQDAP 135
QY 61 DTHYVVSEPLGRKSKYERLFPYRPDQVSADVSYDDGCEPCGNDTFRREPAIVRFS 120
DB 136 DTHYVVSEPLGRKSKYERLFPYRPDQVSADVSYDDGCEPCGNDTFRREPAIVRFS 195
QY 121 RFTVEFEAIVPLHAAPGDAVAEIDALYDVLVQEKWGLDVMLMGDFNAGCSYVRPSQ 180
DB 196 RFTVEFEAIVPLHAAPGDAVAEIDALYDVLVQEKWGLDVMLMGDFNAGCSYVRPSQ 255
QY 181 WSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPSALPFFNQAYG 240
DB 256 WSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPSALPFFNQAYG 315
QY 241 LSDQLAQALSDHYFVVEVMLK 260
DB 316 LSDQLAQALSDHYFVVEVMLK 335

RESULT 10
US-08-663-831-2
Sequence 2, Application US/08663831
Patent No. 6391607
GENERAL INFORMATION:
APPLICANT: Lazarus, Robert A.
APPLICANT: Pan, Clark Qun
TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,831

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; FILING DATE: 415/952-9881
; TELEFAX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-663-831-3

Query Match          99.3%; Score 1358; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 4e-150;
Matches 258; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLVSIIQILSRVDIALVQEVDRDHLTAAGKLLDNLNQDAP 60
DB 1 LKIAAFNIQTGETKMSNATLVSIIQILSRVDIALVQEVDRDHLTAAGKLLDNLNQDAP 60

QY 61 DTHYVWSEPLGRKSYKERYLFVYRPDQVSAVDSSYYDDGCEPCGNDTFNREPAIVRFFS 120
DB 61 DTHYVWSEPLGRKSYKERYLFVYRPDQVSAVDSSYYDDGCEPCGNDTFNREPAIVRFFS 120

QY 121 RFEVREFAIVPLHAAPGDVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
DB 121 RFEVREFAIVPLHAAPGDVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180

QY 181 WSSIRLWTSPTQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAIVVPSALPFNFQAAAYG 240
DB 181 WSSIRLWTSPTQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAIVVPSALPFNFQAAAYG 240

QY 241 LSDQLAQAIISDHYPVEVWMLK 260
DB 241 LSDQLAQAIISDHYPVEVWMLK 260

RESULT 12
US-08-663-831-11
; Sequence 11, Application US/08663831
; Patent No. 6391607
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,831
; FILING DATE: 14-Jun-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELETYPE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-663-831-11

```

```

; FILING DATE: 14-Jun-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELETYPE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-663-831-2

Query Match          99.3%; Score 1358; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 4e-150;
Matches 258; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLVSIIQILSRVDIALVQEVDRDHLTAAGKLLDNLNQDAP 60
DB 1 LKIAAFNIQTGETKMSNATLVSIIQILSRVDIALVQEVDRDHLTAAGKLLDNLNQDAP 60

QY 61 DTHYVWSEPLGRKSYKERYLFVYRPDQVSAVDSSYYDDGCEPCGNDTFNREPAIVRFFS 120
DB 61 DTHYVWSEPLGRKSYKERYLFVYRPDQVSAVDSSYYDDGCEPCGNDTFNREPAIVRFFS 120

QY 121 RFEVREFAIVPLHAAPGDVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
DB 121 RFEVREFAIVPLHAAPGDVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180

QY 181 WSSIRLWTSPTQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAIVVPSALPFNFQAAAYG 240
DB 181 WSSIRLWTSPTQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAIVVPSALPFNFQAAAYG 240

QY 241 LSDQLAQAIISDHYPVEVWMLK 260
DB 241 LSDQLAQAIISDHYPVEVWMLK 260

RESULT 11
US-08-663-831-3
; Sequence 3, Application US/08663831
; Patent No. 6391607
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,831
; FILING DATE: 14-Jun-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELETYPE: 910/371-7168
;
US-08-663-831-3

```

Query Match 99.3%; Score 1358; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 4e-150;
Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGFTKMSNATLSYIVQILSRVDIALVQVVRDRLTAVGKLLDNLNQDAP 60
DB 1 LKIAAFNIQTGFTKMSNATLSYIVQILSRVDIALVQVVRDRLTAVGKLLDNLNQDAP 60

QY 61 DTHYVWSEPLGRKSKERYLFFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRPS 120
DB 61 DTHYVWSEPLGRKSKERYLFFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRPS 120

QY 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
DB 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180

QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFFNQAA 240
DB 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFFNQAA 240

QY 241 LSDQLAQALSDHPYVEMLK 260
DB 241 LSDQLAQALSDHPYVEMLK 260

RESULT 13

US-08-663-831-15
; Sequence 15, Application US/08663831
; Patent No. 6391607
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Pan, Clark Qun
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,831
; FILING DATE: 14-Jun-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1042
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-663-831-15

Query Match 99.3%; Score 1358; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 4e-150;
Matches 258; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGFTKMSNATLSYIVQILSRVDIALVQVVRDRLTAVGKLLDNLNQDAP 60
DB 1 LKIAAFNIQTGFTKMSNATLSYIVQILSRVDIALVQVVRDRLTAVGKLLDNLNQDAP 60

QY 61 DTHYVWSEPLGRKSKERYLFFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRPS 120
DB 61 DTHYVWSEPLGRKSKERYLFFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRPS 120

QY 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
DB 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180

QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFFNQAA 240
DB 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFFNQAA 240

QY 241 LSDQLAQALSDHPYVEMLK 260
DB 241 LSDQLAQALSDHPYVEMLK 260

RESULT 14

US-08-663-831-4
; Sequence 4, Application US/08663831
; Patent No. 6391607
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Pan, Clark Qun
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,831
; FILING DATE: 14-Jun-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1042
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-663-831-4

Query Match 99.3%; Score 1357; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 5.2e-150;
Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGFTKMSNATLSYIVQILSRVDIALVQVVRDRLTAVGKLLDNLNQDAP 60
DB 1 LKIAAFNIQTGFTKMSNATLSYIVQILSRVDIALVQVVRDRLTAVGKLLDNLNQDAP 60

QY 61 DTHYVWSEPLGRKSKERYLFFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRPS 120
DB 61 DTHYVWSEPLGRKSKERYLFFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRPS 120

QY 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
DB 121 RFEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: November 21, 2003, 13:56:42 ; Search time 30 Seconds
(without alignments)
1582.182 Million cell updates/sec

Title: US-10-005-306-9
Perfect score: 1367
Sequence: 1 LKTAARNIQFTGKMSNAT.....LSQLAQASHDYHVEVWLK 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1367	100.0	260	14	US-10-005-306-9
2	1364	99.8	260	14	US-10-005-306-10
3	1362	99.6	260	14	US-09-825-012-3
4	1362	99.6	260	14	US-10-133-065-4
5	1362	99.6	260	14	US-10-074-509-4
6	1362	99.6	260	14	US-10-005-306-1
7	1362	99.6	260	14	US-10-005-306-14
8	1362	99.6	260	15	US-10-005-675-14
9	1362	99.6	282	10	US-09-825-012-1
10	1362	99.6	341	15	US-10-005-675-13
11	1362	99.6	346	15	US-10-155-407A-1
12	1362	99.6	515	10	US-09-825-012-66
13	1362	99.6	517	10	US-09-825-012-38
14	1362	99.6	519	10	US-09-825-012-76
15	1362	99.6	521	10	US-09-825-012-71

Sequence 85, Appl	525	10	US-09-825-012-85
Sequence 43, Appl	527	10	US-09-825-012-43
Sequence 95, Appl	529	10	US-09-825-012-95
Sequence 90, Appl	531	10	US-09-825-012-90
Sequence 52, Appl	729	10	US-09-825-012-52
Sequence 49, Appl	730	10	US-09-825-012-49
Sequence 46, Appl	731	10	US-09-825-012-46
Sequence 61, Appl	739	10	US-09-825-012-61
Sequence 58, Appl	740	10	US-09-825-012-58
Sequence 55, Appl	741	10	US-09-825-012-55
Sequence 2, Appl	260	14	US-10-005-306-2
Sequence 3, Appl	260	14	US-10-005-306-3
Sequence 11, Appl	260	14	US-10-005-306-11
Sequence 15, Appl	260	14	US-10-005-306-15
Sequence 4, Appl	260	14	US-10-005-306-4
Sequence 5, Appl	260	14	US-10-005-306-5
Sequence 6, Appl	260	14	US-10-005-306-6
Sequence 12, Appl	260	14	US-10-005-306-12
Sequence 13, Appl	260	14	US-10-005-306-13
Sequence 16, Appl	260	14	US-10-005-306-16
Sequence 8, Appl	260	14	US-10-005-306-8
Sequence 7, Appl	260	14	US-10-005-306-7
Sequence 17, Appl	260	14	US-10-005-306-17
Sequence 15, Appl	260	15	US-10-005-675-15
Sequence 5, Appl	161	10	US-09-825-012-5
Sequence 3, Appl	285	14	US-10-133-065-3
Sequence 2, Appl	305	14	US-10-074-509-3
Sequence 2, Appl	305	14	US-10-133-065-2
Sequence 2, Appl	305	14	US-10-074-509-2

ALIGNMENTS

RESULT 1
US-10-005-306-9
; Sequence 9, Application US/10005306
; Publication No. US20020173025A1
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Pan, Clark Qun
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; FILE REFERENCE: F1042C1
; CURRENT APPLICATION NUMBER: US/10/005,306
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 08/663,831
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-306-9

Query Match	100.0%	Score 1367;	DB 14;	Length 260;
Best Local Similarity	100.0%;	Pred. No. 5e-145;		
Matches 260;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	LKTAARNIQFTGKMSNATLSVIVQILSRIDYALVQEVDRDHLTAGVKLLDNLNODAP	60	
Db	1	LKTAARNIQFTGKMSNATLSVIVQILSRIDYALVQEVDRDHLTAGVKLLDNLNODAP	60	
Qy	61	DTYHYVSEPLGRKSYKERYLFVYRPDQVSANDSVYYDDGCEPCGNDTFNREPAIVRFFS	120	
Db	61	DTYHYVSEPLGRKSYKERYLFVYRPDQVSANDSVYYDDGCEPCGNDTFNREPAIVRFFS	120	
Qy	121	RFTVREFAIVPLHAAPGDAVAEIDALYDYLVDQEKWGLDVMMDGFNAGCSYVRPSQ	180	
Db	121	RFTVREFAIVPLHAAPGDAVAEIDALYDYLVDQEKWGLDVMMDGFNAGCSYVRPSQ	180	
Qy	181	WSSTRLWTSPTFQWLIPDSADTTATPHCAVDRTVAGMLLRGAIVVPDSALPFNFQAYG	240	

Db 181 WSSIRLWTSPTFQWLIPDSADTTATPHCAVDRIIVAGMLLRGAVVPSALPFFNQAYG 240
QY 241 LSDQLAQAI SDHYPEVWMLK 260
Db 241 LSDQLAQAI SDHYPEVWMLK 260

RESULT 2
US-10-005-306-10
; Sequence 10, Application US/10005306
; Publication No. US20020173025A1
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Pan, Clark Qun
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; FILE REFERENCE: P1042C1
; CURRENT APPLICATION NUMBER: US/10/005,306
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 08/663,831
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 10
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-306-10

Query Match 99.8%; Score 1364; DB 14; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.1e-144;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGCTKMSNATLSYIVQILSRDYDIALVQEVDRDLSHTAVGKLLDNLNODAP 60
Db 1 LKIAAFNIQTGCTKMSNATLSYIVQILSRDYDIALVQEVDRDLSHTAVGKLLDNLNODAP 60

QY 61 DTYHVVSEPLGRKSKYKERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120
Db 61 DTYHVVSEPLGRKSKYKERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120

QY 121 RTEVREFAIPLHAAPGDAVAEIDALYDVLVQEKWGLDVMGMDFNAGCSYVRPSQ 180
Db 121 RTEVREFAIPLHAAPGDAVAEIDALYDVLVQEKWGLDVMGMDFNAGCSYVRPSQ 180

QY 181 WSSIRLWTSPTFQWLIPDSADTTATPHCAVDRIIVAGMLLRGAVVPSALPFFNQAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPHCAVDRIIVAGMLLRGAVVPSALPFFNQAYG 240

RESULT 3
US-09-825-012-3
; Sequence 3, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-012-3

Query Match 99.6%; Score 1362; DB 10; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.8e-144;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGCTKMSNATLSYIVQILSRDYDIALVQEVDRDLSHTAVGKLLDNLNODAP 60
Db 1 LKIAAFNIQTGCTKMSNATLSYIVQILSRDYDIALVQEVDRDLSHTAVGKLLDNLNODAP 60

QY 61 DTYHVVSEPLGRKSKYKERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120
Db 61 DTYHVVSEPLGRKSKYKERYLFVYRPDQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120

QY 121 RTEVREFAIPLHAAPGDAVAEIDALYDVLVQEKWGLDVMGMDFNAGCSYVRPSQ 180
Db 121 RTEVREFAIPLHAAPGDAVAEIDALYDVLVQEKWGLDVMGMDFNAGCSYVRPSQ 180

QY 181 WSSIRLWTSPTFQWLIPDSADTTATPHCAVDRIIVAGMLLRGAVVPSALPFFNQAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPHCAVDRIIVAGMLLRGAVVPSALPFFNQAYG 240

QY 241 LSDQLAQAI SDHYPEVWMLK 260
Db 241 LSDQLAQAI SDHYPEVWMLK 260

RESULT 4
US-10-133-065-4
; Sequence 4, Application US/10133065
; Publication No. US20020123122A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; TITLE OF INVENTION: HUMAN DNASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/133,065
; FILING DATE: 26-Apr-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/643,520
; FILING DATE: 22/08/2000
; APPLICATION NUMBER: 08/794827
; FILING DATE: 04-Feb-1997
; APPLICATION NUMBER: 60/109796
; FILING DATE: 05-Feb-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W
; REGISTRATION NUMBER: C.F.R. 10.9(b)
; REFERENCE/DOCKET NUMBER: P1000R1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-133-065-4

Query Match 99.6%; Score 1362; DB 14; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.8e-144;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQDAP 60
Db 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQDAP 60

Qy 61 DTHYVVSSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
Db 61 DTHYVVSSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120

Qy 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
Db 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180

Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFFNQAAAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFFNQAAAYG 240

Qy 241 LSDQLAQAIISDHYPEVWMLK 260
Db 241 LSDQLAQAIISDHYPEVWMLK 260

RESULT 5

US-10-074-509-4

; Sequence 4, Application US/10074509

; Publication No. US20020142437A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Baron, Will F.

; TITLE OF INVENTION: HUMAN DNASE

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA: US/10/074,509

; FILING DATE: 11-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/643,520

; FILING DATE: 22/08/2000

; APPLICATION NUMBER: 08/794827

; FILING DATE: 04-Feb-1997

; APPLICATION NUMBER: 60/109796

; FILING DATE: 05-Feb-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Johnston, Sean A.

; REGISTRATION NUMBER: 35,910

; REFERENCE/DOCKET NUMBER: P1000R1C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-3562

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 260 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-074-509-4

Query Match 99.6%; Score 1362; DB 14; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.8e-144;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQDAP 60
Db 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQDAP 60

Qy 61 DTHYVVSSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
Db 61 DTHYVVSSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120

Qy 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
Db 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180

Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFFNQAAAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFFNQAAAYG 240

Qy 241 LSDQLAQAIISDHYPEVWMLK 260
Db 241 LSDQLAQAIISDHYPEVWMLK 260

RESULT 6

US-10-005-306-1

; Sequence 1, Application US/10005306

; Publication No. US20020173025A1

; GENERAL INFORMATION:

; APPLICANT: Lazarus, Robert A.

; APPLICANT: Pan, Clark Qun

; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS

; FILE REFERENCE: P1042C1

; CURRENT APPLICATION NUMBER: US/10/005,306

; CURRENT FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US 08/663,831

; PRIOR FILING DATE: 1996-06-14

; NUMBER OF SEQ ID NOS: 17

; SEQ ID NO 1

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-005-306-1

Query Match 99.6%; Score 1362; DB 14; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.8e-144;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQDAP 60
Db 1 LKIAAFNIQTGCTKMSNATLVSYIVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQDAP 60

Qy 61 DTHYVVSSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
Db 61 DTHYVVSSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120

Qy 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180
Db 121 RFTVEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ 180

Qy 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFFNQAAAYG 240
Db 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSALPFFNQAAAYG 240

Qy 241 LSDQLAQAIISDHYPEVWMLK 260
Db 241 LSDQLAQAIISDHYPEVWMLK 260

RESULT 7

US-10-005-306-14

; Sequence 14, Application US/10005306

```

; Publication No. US20020173025A1
; GENERAL INFORMATION: Robert A.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
; FILE REFERENCE: P1042C1
; CURRENT APPLICATION NUMBER: US/10/005,306
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 08/663,831
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 14
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-306-14

Query Match 99.6%; Score 1362; DB 14; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.8e-144;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLVSIYVQLSKYDIALVQEVDRDLSHTAVGKLLDNQDAP 60
DB 1 LKIAAFNIQTGETKMSNATLVSIYVQLSKYDIALVQEVDRDLSHTAVGKLLDNQDAP 60

QY 61 DTYHVVSEPLGRKSYKERYLFVTRPQVSAVDSYDDGCEPCGNDTFNREPAIVRFS 120
DB 61 DTYHVVSEPLGRKSYKERYLFVTRPQVSAVDSYDDGCEPCGNDTFNREPAIVRFS 120

QY 121 RFTVEVREPAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
DB 121 RFTVEVREPAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180

QY 181 WSSIRLWTSPTFQMLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSDLPNFOAAYG 240
DB 181 WSSIRLWTSPTFQMLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSDLPNFOAAYG 240

QY 241 LSDQLAQAISSDHPVVEVWLK 260
DB 241 LSDQLAQAISSDHPVVEVWLK 260

RESULT 8
US-10-005-675-14
; Sequence 14, Application US/10005675
; Publication No. US20030044403A1
; GENERAL INFORMATION:
; APPLICANT: Shak, Steven
; TITLE OF INVENTION: Anti-Infective Therapy
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinRatIn (Genentech)
; CURRENT APPLICATION DATA: US/10/005,675
; APPLICATION NUMBER: US/10/005,675
; FILING DATE: 07-NOV-03
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/669306
; FILING DATE: 25-Sep-2001
; APPLICATION NUMBER: 08/873506
; FILING DATE: 08-Dec-1999
; APPLICATION NUMBER: 08/643195
; FILING DATE: 06-May-1996

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; APPLICATION NUMBER: 08/459909
; FILING DATE: 02-Jun-1995
; APPLICATION NUMBER: 08/191749
; FILING DATE: 03-Feb-1994
; APPLICATION NUMBER: 07/914,226
; FILING DATE: 13-Jul-1992
; APPLICATION NUMBER: 07/448038
; FILING DATE: 08-Dec-1989
; APPLICATION NUMBER: 07/289958
; FILING DATE: 23-Dec-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P0530P1C10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3562
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-005-675-14

Query Match 99.6%; Score 1362; DB 15; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.8e-144;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLVSIYVQLSKYDIALVQEVDRDLSHTAVGKLLDNQDAP 60
DB 1 LKIAAFNIQTGETKMSNATLVSIYVQLSKYDIALVQEVDRDLSHTAVGKLLDNQDAP 60

QY 61 DTYHVVSEPLGRKSYKERYLFVTRPQVSAVDSYDDGCEPCGNDTFNREPAIVRFS 120
DB 61 DTYHVVSEPLGRKSYKERYLFVTRPQVSAVDSYDDGCEPCGNDTFNREPAIVRFS 120

QY 121 RFTVEVREPAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180
DB 121 RFTVEVREPAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLDVMGMDFNAGCSYVRPSQ 180

QY 181 WSSIRLWTSPTFQMLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSDLPNFOAAYG 240
DB 181 WSSIRLWTSPTFQMLIPDSADTTATPTHCAYDRIVVAGMLRGAVVPSDLPNFOAAYG 240

QY 241 LSDQLAQAISSDHPVVEVWLK 260
DB 241 LSDQLAQAISSDHPVVEVWLK 260

RESULT 9
US-09-825-012-1
; Sequence 1, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-012-1

Query Match 99.6%; Score 1362; DB 10; Length 282;

```

Best Local Similarity 99.6%; Pred. No. 2e-144;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKIAAFNIQTGETKMSNATLSYIVQILSRDYIALVOEVRDSDSHLTAVGKLLDNLNQDAP 60
DB 23 LKIAAFNIQTGETKMSNATLSYIVQILSRDYIALVOEVRDSDSHLTAVGKLLDNLNQDAP 82
QY 61 DTYHYVVSSEPLGRKSYKERYLFVYRDPQVSAVDSVYDDGCEPCGNDTFNREPAIVRPF 120
DB 83 DTYHYVVSSEPLGRKSYKERYLFVYRDPQVSAVDSVYDDGCEPCGNDTFNREPAIVRPF 142
QY 121 RFTVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMGDFNAGCSYVRPSQ 180
DB 143 RFTVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMGDFNAGCSYVRPSQ 202
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLRGAVVPSALPFFNFOAAYG 240
DB 203 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLRGAVVPSALPFFNFOAAYG 262
QY 241 LSDQLAQALSDHYPVEVWMLK 260
DB 263 LSDQLAQALSDHYPVEVWMLK 282

RESULT 10

US-10-005-675-13
; Sequence 13, Application US/10005675
; Publication No. US2003004403A1

GENERAL INFORMATION:

APPLICANT: Shak, Steven
TITLE OF INVENTION: Anti-Infective Therapy
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/005,675
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/669306
FILING DATE: 25-Sep-2001
APPLICATION NUMBER: 08/873506
FILING DATE: 08-Dec-1999
APPLICATION NUMBER: 08/643195
FILING DATE: 06-May-1996
APPLICATION NUMBER: 08/459909
FILING DATE: 02-Jun-1995
APPLICATION NUMBER: 08/191749
FILING DATE: 03-Feb-1994
APPLICATION NUMBER: 07/914,226
FILING DATE: 13-Jul-1992
APPLICATION NUMBER: 07/448038
FILING DATE: 08-Dec-1989
APPLICATION NUMBER: 07/289958
FILING DATE: 23-Dec-1988

ATTORNEY/AGENT INFORMATION:

NAME: Johnston, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: P0530P1C10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3562
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-005-675-13

Query Match 99.6%; Score 1362; DB 15; Length 341;
Best Local Similarity 99.6%; Pred. No. 2.7e-144;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLSYIVQILSRDYIALVOEVRDSDSHLTAVGKLLDNLNQDAP 60
DB 73 LKIAAFNIQTGETKMSNATLSYIVQILSRDYIALVOEVRDSDSHLTAVGKLLDNLNQDAP 132
QY 61 DTYHYVVSSEPLGRKSYKERYLFVYRDPQVSAVDSVYDDGCEPCGNDTFNREPAIVRPF 120
DB 133 DTYHYVVSSEPLGRKSYKERYLFVYRDPQVSAVDSVYDDGCEPCGNDTFNREPAIVRPF 192
QY 121 RFTVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMGDFNAGCSYVRPSQ 180
DB 193 RFTVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLDVMGMGDFNAGCSYVRPSQ 252
QY 181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLRGAVVPSALPFFNFOAAYG 240
DB 253 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIIVVAGMLRGAVVPSALPFFNFOAAYG 312
QY 241 LSDQLAQALSDHYPVEVWMLK 260
DB 313 LSDQLAQALSDHYPVEVWMLK 332

RESULT 11

US-10-155-407A-1

; Sequence 1, Application US/10155407A
; Publication No. US20030077267A1
; GENERAL INFORMATION:

APPLICANT: Frenz, John
Shire, Steven J.
Sliwkowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/155,407A
FILING DATE: 22-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/638112
FILING DATE: 11-Aug-2000
APPLICATION NUMBER: 08/942561
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: 08/634125
FILING DATE: 19-Apr-1996
APPLICATION NUMBER: 08/409631
FILING DATE: 22-Mar-1995
APPLICATION NUMBER: 08/348284
FILING DATE: 30-Nov-2003
APPLICATION NUMBER: 08/116186
FILING DATE: 02-Sep-1993
APPLICATION NUMBER: 07/895300
FILING DATE: 08-Jun-1992

ATTORNEY/AGENT INFORMATION:

NAME: Evans, David W.

REGISTRATION NUMBER: NONE

REFERENCE/DOCKET NUMBER: P0747C8

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1739

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 346 amino acids

TYPE: Amino acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-155-407A-1

Query Match 99.6%; Score 1362; DB 15; Length 346;
Best Local Similarity 99.6%; Pred. No. 2.8e-144;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLSVIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 60

DB 76 LKIAAFNIQTGETKMSNATLSVIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 135

QY 61 DTYHYVWSEPLGRNSYKERYLFVYRPQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120

DB 136 DTYHYVWSEPLGRNSYKERYLFVYRPQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 195

QY 121 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVOEKWGLEDMVMGDFNAGCSYVRPSQ 180

DB 196 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVOEKWGLEDMVMGDFNAGCSYVRPSQ 255

QY 181 WSSIRLMTSPTFFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVPDPSALPNFQAAYG 240

DB 256 WSSIRLMTSPTFFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVPDPSALPNFQAAYG 315

QY 241 LSDQLAQAI SDHYPEVWMLK 260

DB 316 LSDQLAQAI SDHYPEVWMLK 335

RESULT 12

US-09-825-012-66

Sequence 66, Application US/09825012

Patent No. US20020122798A1

GENERAL INFORMATION:

APPLICANT: Young, Robert

TITLE OF INVENTION: Compounds for Targeting

FILE REFERENCE: 43191-256808

CURRENT APPLICATION NUMBER: US/09/825,012

CURRENT FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/237,159

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: GB 0008049.9

PRIOR FILING DATE: 2000-04-03

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.1

SEQ ID NO 66

LENGTH: 515

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion

US-09-825-012-66

Query Match

Best Local Similarity 99.6%; Score 1362; DB 10; Length 515;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLSVIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 60

DB 256 LKIAAFNIQTGETKMSNATLSVIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 315

QY 61 DTYHYVWSEPLGRNSYKERYLFVYRPQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120

DB 316 DTYHYVWSEPLGRNSYKERYLFVYRPQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 375

QY 121 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVOEKWGLEDMVMGDFNAGCSYVRPSQ 180

DB 376 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVOEKWGLEDMVMGDFNAGCSYVRPSQ 435

QY 181 WSSIRLMTSPTFFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVPDPSALPNFQAAYG 240

DB 436 WSSIRLMTSPTFFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVPDPSALPNFQAAYG 495

QY 241 LSDQLAQAI SDHYPEVWMLK 260

DB 496 LSDQLAQAI SDHYPEVWMLK 515

RESULT 13

US-09-825-012-38

Sequence 38, Application US/09825012

Patent No. US20020122798A1

GENERAL INFORMATION:

APPLICANT: Young, Robert

TITLE OF INVENTION: Compounds for Targeting

FILE REFERENCE: 43191-256808

CURRENT APPLICATION NUMBER: US/09/825,012

CURRENT FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/237,159

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: GB 0008049.9

PRIOR FILING DATE: 2000-04-03

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.1

SEQ ID NO 38

LENGTH: 517

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion

US-09-825-012-38

Query Match

Best Local Similarity 99.6%; Score 1362; DB 10; Length 517;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKIAAFNIQTGETKMSNATLSVIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 60

DB 258 LKIAAFNIQTGETKMSNATLSVIVQILSRDYIALVQEVDRDLSHLTAVGKLLDNLNQDAP 317

QY 61 DTYHYVWSEPLGRNSYKERYLFVYRPQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 120

DB 318 DTYHYVWSEPLGRNSYKERYLFVYRPQVSAVDSYVYDDGCEPCGNDTFNREPAIVRFFS 377

QY 121 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVOEKWGLEDMVMGDFNAGCSYVRPSQ 180

DB 378 RFTVREFAIVPLHAAPGDAVAEIDALYDYLVOEKWGLEDMVMGDFNAGCSYVRPSQ 437

QY 181 WSSIRLMTSPTFFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVPDPSALPNFQAAYG 240

DB 438 WSSIRLMTSPTFFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVPDPSALPNFQAAYG 497

QY 241 LSDQLAQAI SDHYPEVWMLK 260

DB 498 LSDQLAQAI SDHYPEVWMLK 517

RESULT 14

US-09-825-012-76

Sequence 76, Application US/09825012

Patent No. US20020122798A1

GENERAL INFORMATION:

APPLICANT: Young, Robert

TITLE OF INVENTION: Compounds for Targeting

FILE REFERENCE: 43191-256808

; CURRENT APPLICATION NUMBER: US/09/825,012
 ; CURRENT FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/237,159
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: GB 0008049.9
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 76
 ; TYPE: PRT
 ; LENGTH: 519
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Humanised HMFGL Fd - DNase I fusion
 ; US-09-825-012-76

Query Match 99.6%; Score 1362; DB 10; Length 519;
 Best Local Similarity 99.6%; Pred. No. 5e-144;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	LKTAENIOTFGETKMSNATLVSYIVQILSRDYDIALVOEVRDLSHLTAVGKLLDNLNDAP	60
DB	260	LKTAENIOTFGETKMSNATLVSYIVQILSRDYDIALVOEVRDLSHLTAVGKLLDNLNDAP	319
QY	61	DTYHYVVSPLGRKSYKERYLFVYRPDQVSAVDSSYYDDGCEPCGNDTFNREPAIVRFFS	120
DB	320	DTYHYVVSPLGRKSYKERYLFVYRPDQVSAVDSSYYDDGCEPCGNDTFNREPAIVRFFS	379
QY	121	RTEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ	180
DB	380	RTEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ	439
QY	181	WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAVG	240
DB	440	WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAVG	499
QY	241	LSDQLAQAISSDHYVVEVWLK	260
DB	500	LSDQLAQAISSDHYVVEVWLK	519

RESULT 15

US-09-825-012-71
 ; Sequence 71, Application US/09825012
 ; Patent No. US2002012798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Robert
 ; TITLE OF INVENTION: Compounds for Targeting
 ; FILE REFERENCE: 43191-256808
 ; CURRENT APPLICATION NUMBER: US/09/825,012
 ; CURRENT FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/237,159
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: GB 0008049.9
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 71
 ; LENGTH: 521
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Humanised HMFGL Fd - DNase I fusion
 ; US-09-825-012-71

Query Match 99.6%; Score 1362; DB 10; Length 521;
 Best Local Similarity 99.6%; Pred. No. 5e-144;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	LKTAENIOTFGETKMSNATLVSYIVQILSRDYDIALVOEVRDLSHLTAVGKLLDNLNDAP	60
DB	262	LKTAENIOTFGETKMSNATLVSYIVQILSRDYDIALVOEVRDLSHLTAVGKLLDNLNDAP	321

QY	61	DTYHYVVSPLGRKSYKERYLFVYRPDQVSAVDSSYYDDGCEPCGNDTFNREPAIVRPPS	120
DB	322	DTYHYVVSPLGRKSYKERYLFVYRPDQVSAVDSSYYDDGCEPCGNDTFNREPAIVRPPS	381
QY	121	RTEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ	180
DB	382	RTEVREFAIVPLHAAPGDAVAEIDALYDVLDVQEKWGLEDMVLMGDFNAGCSYVRPSQ	441
QY	181	WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAVG	240
DB	442	WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAVG	501
QY	241	LSDQLAQAISSDHYVVEVWLK	260
DB	502	LSDQLAQAISSDHYVVEVWLK	521

Search completed: November 21, 2003, 14:02:04
 Job time : 31 secs